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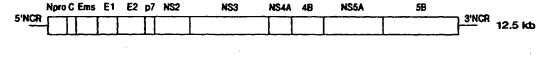
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(54) Title: HCV/BVDV CHIMERIC GENOMES AND USES THEREOF

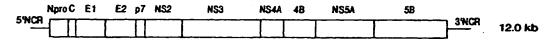
BVDV-NADL



HCV-H77C



HCV/BVDV (Chimeric RNA)



(57) Abstract: The present invention relates to molecular approaches to the production of nucleic acid sequences which comprise the genomes of chimeric hepatitis C virus-bovine viral diarrhea viruses (HCV-BVDV). The invention also relates to the use of these chimeric nucleic acid sequences to produce chimeric virions in cells and the use of these chimeric virions in HCV antibody neutralization assays, and for the development of vaccines and therapeutics for HCV.



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TITLE OF INVENTION

HCV/BVDV Chimeric Genomes and Uses Thereof

FIELD OF INVENTION

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The present invention relates to molecular approaches to the production of nucleic acid sequences which comprise the genomes of chimeric hepatitis C virus-bovine viral diarrhea viruses (HCV-BVDV). The invention also relates to the use of these chimeric nucleic acid sequences to produce chimeric virions in cells and the use of these chimeric virions in HCV antibody neutralization assays, and for the development of vaccines and therapeutics for HCV.

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Background Of Invention

Hepatitis C virus (HCV) has a positive-sense single-strand RNA genome and is a member of the genus Hepacivirus within the Flaviviridae family of viruses (Rice, 1996). As for all positive-stranded RNA viruses, the genome of HCV functions as mRNA from which all viral proteins necessary for propagation are translated.

The viral genome of HCV is approximately 9600 nucleotides (nts) in length and consists of a highly conserved 5' untranslated region (UTR), a single long open reading frame (ORF) of approximately 9,000 nts and a complex 3' UTR. The 5' UTR contains an internal ribosomal entry site (Tsukiyama-Kohara et al., 1992; Honda et al., 1996). The 3' UTR consists of a short variable region, a polypyrimidine tract of variable length and, at the 3' end, a highly conserved region of approximately 100 nucleotides (Kolykhalov et al., 1996;

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accounts for the majority of HCV infections but genotypes 2 and 3 each account for 5-15%.

At present, more than 80% of individuals infected with HCV become chronically infected and these chronically infected individuals have a relatively high risk of developing chronic hepatitis, liver cirrhosis and hepatocellular carcinoma (Hoofnagle, 1997). The only effective therapy for chronic hepatitis C, interferon (IFN), alone or in combination with ribavirin, induces a sustained response in less than 50% of treated patients (Davis et al., 1998; McHutchinson et al., 1998). Consequently, HCV is currently the most common cause of end stage liver failure and the reason for about 30% of liver transplants performed in the U.S. (Hoofnagle, 1997). In addition, a number of recent studies suggested that the severity of liver disease and the outcome of therapy may be genotype-dependent (reviewed in Bukh et al., 1997). In particular, these studies suggested that infection with HCV genotype 1b was associated with more severe liver disease (Brechot, 1997) and a poorer response to IFN therapy (Fried and Hoofnagle, 1995). As a result of the inability to develop a universally effective therapy against HCV infection, it is estimated that there are still more than 25,000 new infections yearly in the U.S. (Alter Moreover, since there is no vaccine for HCV, HCV remains a serious public health problem.

Despite the intense interest in the development of vaccines and therapies for HCV, progress has been hindered by the absence of a useful cell culture system for laboratory study (2-7). For example, although the virus has been grown in some cell lines,

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chimeric nucleic acid sequences to study the molecular properties of HCV indirectly in vitro.

The present invention also relates to the polypeptides encoded by the chimeric nucleic acid sequences of the invention or fragments thereof.

The invention also provides that the chimeric nucleic acid sequences and the chimeric viruses of the invention be supplied in the form of a kit, alone or in the form of a pharmaceutical composition.

DESCRIPTION OF FIGURES

Fig. 1. Genomic organization of BVDV, HCV and HCV/BVDV chimera. The BVDV and HCV are NADL (14, 21) and H77 strains (12), respectively. The complete BVDV-NADL genome consists of, in 5' to 3' order, 5'NCR (nucleotides 1-385), N^{pro} (nucleotides 386-889), Core (nucleotides 890-1195), E^{rns} (nucleotides 1196-1876), E1 (nucleotides 1877-2461), E2 (nucleotides 2462-3583), P7 and nonstructural genes (nucleotides 3584-12349) and 3'NCR (nucleotides 12352-12578).

Fig. 2. Strategy for the construction of chimeric cDNA, pHCV/BVDV-3, which has core, El and E2 of HCV in the backbone of BVDV. The fusion PCR products were cloned into pBV18-F2 after digestion with *SnaB* I and *Bsm* I. The fragments containing fusion PCR products were cloned into pSDMlu-3' after digestion with *Cla* I and *Dra* III.

Figures 3A-3H show the nucleotide and deduced amino acid sequences of the infectious HCV clone of genotype la.

Figures 4A-4H show the nucleotide and deduced amino acid sequences of the infectious clone of genotype

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constructed. Such chimeras can be used to determine the relative importance of E1 or E2 for infection of cell lines. In another embodiment, HCV/BVDV chimeras in which one of the nonstructural genes of BVDV, such as NS3 RNA helicase, NS3 protease, or the NS5B RNA-dependent RNA polymerase are replaced by the corresponding non-structural genes of HCV may be constructed. Such chimeras would, for example, be useful in identifying inhibitors of viral enzyme activity which would be useful as antiviral agents.

In yet another embodiment, hypervariable region 1 (HVR1) from multiple HCV genotypes may be combined into one HCV/BVDV chimera. The only limit for constructing this type of chimera is that the viral genome must be able to be packaged. Alternatively, a chimera can be constructed which contain an HVR1 sequence from one HCV genotype. Such chimeras can be used as an inactivated multivalent vaccine or to screen for neutralizing antibodies to multiple HCV genotypes.

The HCV/BVDV chimeras of the invention may be constructed using any HCV and BVDV clones. However, in a preferred embodiment, the HCV clones are infectious HCV clones of genotype la (ATCC accession number PTA-157; Figures 3A-3F), 1b (ATCC accession number 209596; Figures 4A-4F) or 2a (ATCC accession number PTA-153; SEQ ID NOS:3-4) and the infectious BVDV clone pVVNADL are used.

In constructing the chimeric nucleic acid sequences of the invention, it is to be understood that the retention of the E^{rns} gene of BVDV in any chimeric is entirely optional. Thus, when it is stated that the HCV/BVDV chimeras could be constructed in which, for

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the growing of animal cells in vitro and transfecting the cells with the chimeric nucleic acid of the invention, then determining if the cells show indicia of HCV infection. Such indicia include the detection of viral antigens in the cell, for example, by immunofluorescence procedures well known in the art; the detection of viral polypeptides by Western blotting using antibodies specific therefor; and the detection of newly transcribed viral RNA within the cells via methods such as RT-PCR. The presence of live, infectious virus particles following such tests may also be shown by injection of cell culture medium or cell lysates into healthy, susceptible animals, with subsequent exhibition of the signs and symptoms of HCV infection. Alternatively, the presence of live, infectious virus particles following such tests may also be shown by serial passaging the chimeric virus in cells.

Suitable cells or cell lines for culturing the chimeric viruses of the invention include, but are not limited to, EBTr(A) and Huh7.

Preferably, transfection of cells with the chimeric sequences is carried out in the presence of helper BVDV which is preferably of a noncytopathogenic strain. In one embodiment, the cell lines to be infected may already contain a helper BVDV. Such cells include, but are not limited to, EBTr(A).

Alternatively, the cell lines to be transfected may be infected with a helper BVDV prior to, or concurrent with, transfection with the chimeric sequences of the invention.

The present invention also relates to polypeptides encoded by the chimeric nucleic acid

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can then be used to immunize chimpanzees to determine whether the antibodies are protective. Alternatively, cells infected with the chimeric viruses of the invention may be passaged in cell culture to produce attenuated viruses which can be tested as candidate live vaccines. In assaying the ability of the chimeric viruses of the invention to infect mammals one can assay sera or liver of the infected mammal by RT-PCR to determine viral titer. In addition, the virulence phenotype of the virus produced by transfection of mammals with the sequences of the invention can be monitored by methods known in the art such as measurement of liver enzyme levels (alanine aminotransferase (ALT) or isocitrate dehydrogenase (ICD)) or by histopathology of liver biopsies.

Alternatively, mutations may be introduced into the HCV portion of the HCV/BVDV chimeras of the invention in order to enable the production of virions in cell cultures which could then be tested <u>in vivo</u> for improved vaccine properties.

In another embodiment, multiple chimeras containing HCV structural genes (or fragments thereof, such as the HVR1) from multiple genotypes can be administered to generate multivalent vaccines.

When used as a vaccine, the chimeric virions can be administered alone or in a suitable diluent, including, but not limited to, water, saline, or some type of buffered medium. The vaccine according to the present invention may be administered to an animal, especially a mammal, and most especially a human, by a variety of routes, including, but not limited to, intradermally, intramuscularly, subcutaneously, or in

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serum free of BVDV and antibodies to BVDV (Boyt Veternary, Neoshoe, MO) was used. All cells were incubated at 37°C in 5% CO₂.

Table 1
List of Cell Lines

Cell	Origin	Medium
EBTr(A)	Embryonic bovine trachea	10% FBS/MEM
BT	Bovine turbinate	10% horse serum/MEM
MDBK	Bovine kidney	10% horse serum/MEM
EBTr (B)	Embryonic bovine trachea	10% FBS/MEM
Huh 7	human hepatoma	10% FBS/DMEM F12

Antibodies

H79: plasma from patient H obtained in the chronic phase two years after the onset of HCV infection (11); CH1530: serum pool from chimpanzee 1530, obtained in the chronic phase one to two years after the onset of HCV infection. Chimpanzee 1530 became infected with HCV following intrahepatic transfection with pCV-H77C (Yanagi 1997); LMF86 and LMF87: anti-HVR1 (Farci 1996), rabbit anti-peptide sera; Mab NS: anti-BVDV NS3 murine monoclonal antibody kindly provided by Dr. E. Dubovi (Cornell University, Ithaca, NY).

Construction of HCV/BVDV chimeric clone

The C, E1 and E2 genes originating from an infectious clone of the H77 strain of HCV (pCV-H77C, ref. Yanagi 1997), and the backbone originating from two subgenomic plasmids (pBV18-F2 and pSDMlu-3'), used by Vassilev et al. (Vassilev 1997) to generate the infectious clone of the NADL strain of BVDV (pVVNADL), were used to construct the chimeric cDNA clone pHCV-BVDV-3 (ATCC deposit Number PTA-158). The chimeric clone includes sequences corresponding to nucleotides

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HCV/BVDV sequence of the final preparation was determined using standard procedures and about 90 specific sense and antisense primers. Clone pHCV/BVDV-3 was apparently stable since the digestion pattern was as expected following retransformation. The complete sequence differed slightly from the published BVDV sequence of the NADL strain (21), but encoded an intact polyprotein.

Table 2
Oligonucleotides used for PCR amplification

Name	Sequences (5' - 3')	Underline
N-C/H77/S	CAAGTTGCAGCACGAATCCTAAACCTCAAAGAA	N OF BVDV-NADL
Mlul/NADL/S	CACGCGTATCGATGAATTCG	Mlu i
B2-P7/NADL/S	AGCGGAGGCGATTCAGTATGGATCAGGGGAAGTG	E2 OF HCV
E2-P7/H77/R	ATACTGAATCGCCTCCGCTTGGGATATGAG	P7 OF BVDV-NADL
N-C/NADL/R	AGGATTCGTGCTGCAACTTGTGACCCATAGAGGG	Core OF HCV
	CAGTC	
BanI/NADL/R	TACCAGGCTGAGAATGCACTGTAAC	Bsm I
2937S-HCBV	CCTTGTCCACCGGCCTCATCCACCTCCACC	
1353S-NADL	CAATTCATGGTATGATGGATGC	
1419S-NADL	AGTGGAACAAGCATGGTTGGTG	
2335-NADL	CCACGTGGACGAGGCATGCC	
3342R-NADL	CCTGAATCGGCCTTTACCACATCCCCAATC	
1623R-NADL	TTCTTTCCTTTCTTGCAACCTGT	
1590R-NADL	GGGCTATCTCTAGCTTGTGTTAC	
389R-NADL	CCATGTGCCATGTACAGCAGAG	

Transfection of cell lines with transcribed RNA

The plasmid pHCV/BVDV-3 was linearized with SacII (NEB) and treated with T4 DNA polymerase (GIBCO/BRL) to remove the resulting 3' overhang. A truncated form of pHCV/BVDV-3, generated by digestion with HindIII, was used as a negative control. Two micrograms of DNA were transcribed at 37°C for 2 hrs in a 100 µl reaction volume containing 50 U of T7 RNA polymerase (Promega), 10 mM DTT (Promega), 120 U of Rnasin (Promega) and 1 mM rNTPs (GIBCO/BRL). Five microliters of the final reaction mixture was analyzed

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with phosphate buffered saline (PBS) for 10 min. Thereafter, cells were incubated for 20-60 min at 37°C with primary antibodies diluted in 10% bovine serum albumin (BSA) in PBS. As primary antibodies we used an anti-HCV human plasma sample (H79, 1:100 dilution), an anti-HCV chimpanzee serum (CH1530, 1:100 dilution) and an anti-BVDV NS3 monoclonal antibody (Mab-NS, 1:10 dilution). After washing with PBS for 15 min, cells were incubated for 20-40 min at 37°C with secondary antibodies; fluorescein-isothiocyanate (FITC)conjugated goat anti-human antibody (SIGMA) for H79 and CH1530, and rhodamine-conjugated anti-mouse antibody (PIERCE) for anti-BVDV NS3. For double staining, H79 or CH1530 anti-HCV antibody was mixed with the anti-BVDV NS3 monoclonal antibody and incubated on fixed cells as above, followed by washing and incubation with a mixture of both secondary antibodies. After washing, slides were mounted and examined by fluorescence microscopy (Zeiss).

Determination of sucrose gradient density of recovered viruses

with virus stock. At days 9 and 13, respectively, supernatant was harvested. A total of 70 ml of supernatant was layered over 20% sucrose in TN buffer [50mM Tris and 100mM NaCl (pH 7.4)] and centrifuged at 28,000 rpm in an SW28 swinging bucket rotor (Beckman) for 19 hrs at 4°C. The pellet was resuspended in 100 µl of TN buffer. For sucrose equilibrium gradient centrifugation, the resuspended pellet was layered onto a 20-60% (wt/wt) sucrose gradient in TN buffer and centrifuged at 36,000 rpm in an SW40 swinging bucket

incubated with ECL Western blotting detection reagent (Amersham) and exposed to film.

Detection of chimeric genomic RNA by RT-PCR assays

Total RNA was extracted with the TRIzol 5 reagent from 10 or 100 µl of cell suspension, supernatant or material from the sucrose gradient. The RNA pellet was resuspended in 10 mM dithiothreitol (DTT) containing 5% (vol/vol) of RNAsin (20-40 U/µl) 10 (Promega). The RT was performed with avian myeloblastosis virus reverse transcriptase (Promega) and the external anti-sense primer (see below) and PCR was performed with AmpliTaq Gold DNA polymerase (Perkin Elmer) as described (Bukh, 1998a). Specificity was 15 confirmed by sequence analysis of selected DNA products. Each set of experiments included a low titer positive control sample and appropriate negative controls. HCV/BVDV chimeric genomes were detected in one round of 20 PCR with the primers 2937S-HCBV and 3342R-HCBV (Table The structural region of BVDV was detected in an RT-nested PCR with external primers 1353S-NADL and 1623R-NADL and internal primers 1419S-NADL and 1590R-NADL (Table 2). These primers were conserved among all 25 known BVDV strains. Finally, the 5' UTR sequence of BVDV was detected by using universal primers that detect both HCV and BVDV (Bukh 1992, Yanagi 1996), as well as universally conserved BVDV primers (233S-NADL 30 and 389R-NADL). The genome equivalent (GE) titer of HCV, BVDV and HCV/BVDV in positive samples was determined by RT-nested PCR on 10-fold serial dilutions of the extracted RNA (Bukh 1998a). One GE was defined as the number of genomes present in the highest dilution 35

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the Vectastain Elite kit (Vector Laboratories, Burlingame, CA) for peroxidase staining per the manufacturer's directions. The peroxidase substrate kit was Vector VIP (Vector Laboratory). Color development was stopped by washing the slide with water followed by air drying. Foci were counted with the aid of a dissecting microscope.

Focus neutralization assay

The assay was performed exactly as for the focus assay except the 200 µl inoculum consisted of 100 μl of chimeric virus diluted in 10% DMEM, 20 μl undiluted test or control serum, and 80 µl 10% DMEM. Each 200 µl sample was incubated at 4° C in ice overnight prior to inoculation of cells. Sera included fetal calf serum (Boyt) and rabbit pre-immune serum as negative controls, hyperimmune rabbit antisera raised to peptides spanning the HVR1 region of the H27 strain of HCV (Farci, 1996), and goat anti-BVDV (VMRD Pullman, WA) prepared without azide. All sera had been heatinactivated at 56° C for 30 minutes.

Immunofluoresence neutralization assay in Huh7 cells

Two hundred microliters of chimeric virus was mixed with 20 ul of serum or plasma, incubated on ice overnight and added to one well of a four-well chamber slide. After 2 hours at 30° C, 1 ml of agarose overlay was added as for the focus assay. Four days later, 30 slides were fixed and stained as for immunofluoresence microscopy and stained cells were manually counted by scanning the entire well using a Zeis microscope and the 40X objective.

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a particle containing significant amounts of HCV proteins.

Although the proportion of cells producing HCV proteins increased in EBTr(A) cells, it remained low in the MDBK, BT, and EBTr(B) cell lines, suggesting that the virus was not spreading in these cells. In order to determine if these cells were making infectious virus, a homologous transmission was attempted by removing supernatant from each transfected culture and adding it to a new culture of the same cell line. The only successful transmission was from the transfected EBTr(A) cells to naive EBTr(A) cells (Table 3). Therefore. although the chimeric virus genome could replicate in all four cell lines and produced HCV proteins, only in the EBTr(A) cells was virion morphogenesis coupled with availability of a receptor conducive to infection.

Table 3
Homologous passage and heterologous passage

	Transfection	Homologous passage	Heterologous passage
EBTr(A)	+	+	
EBTr (B)	+	-	+
BT	+	-	+
MDBK	+	-	+

Supernatants from transfected cells were passed onto new cells of the same type.

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Two heterologous transmission experiments were performed to determine if the three other cell lines released infectious particles. In the first experiment, supernatant from transfected MDBK cells was inoculated onto the EBTr(A) cells. Immunofluorescence microscopy

Supernatants from transfected EBTr(A) cells were passed to indicated cells.

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RT-PCR primers designed to amplify known BVDV strains were able to amplify a cDNA fragment from uninoculated EBTr(A) cultures (titer: 10^6 GE/ml). The sequence of the cDNA was determined and found to match that of the CP-7 strain of BVDV (18).

Based on the data that only EBTr cells harboring BVDV were able to produce infectious particles containing the chimeric genome, it was hypothesized that the endogenous virus was serving as a helper virus, possibly by providing BVDV structural proteins. order to determine if the infectious chimeric particles contained BVDV glycoproteins, a focus assay was developed in which cells expressing the chimeric genome were identified by their reactivity with CH1530 anti-HCV An infectivity titer of 10⁵ chimeric viruses/ml was obtained for passage 10 virus, which had an RT-PCR titer of 10^8 to 10^9 GE/ml. Chimeric virus produced in EBTr(A) cells was examined for its susceptibility to neutralization by anti-serum to BVDV as compared to neutralization by anti-sera raised against the hypervariable region 1 (HVR1) of the same HCV strain as was in the chimera. Dilutions of chimeric virus were incubated overnight with anti-BVDV, anti-HCV or control sera and the number of infectious particles remaining was determined by the focus assay (Table 4). The number of foci in the rabbit and bovine serum controls decreased in parallel with the dilution factor, indicating that the assay was linear and reliable. The anti-HCV sera did not neutralize the chimera. contrast, anti-BVDV eliminated all foci at each dilution, suggesting that each and every infectious particle contained BVDV glycoproteins and that they were

into these cells might be totally independent of HCV Thirdly, the HCV E2 glycoprotein might glycoprotein. not have folded properly to function or to be recognized by the antibody. The question of the neutralizing potential of the anti-HVR1 serum cannot be answered at 5 this time. By an immunofluoresence microscopy assay, the anti-HVR1 serum had titers of 1:1600 and 1:3200 for rabbits LMF86 and LMF87 respectively but the antibody detected by this assay is not necessarily neutralizing 10 antibody. The functionality of the HCV glycoproteins would best be proved by infecting cells which are not susceptible to infection by BVDV due to an absence of the BVDV receptor. Huh 7 cells were chosen as an experimental system to test for functional HCV 15 glycoproteins because they are a human cell line which grows well and is of hepatocyte origin. Attempts to infect Huh 7 cells with the endogenous BVDV virus of the EBTr(A) cell line were not successful, suggesting either 20 that the receptor for BVDV was absent or that the BVDV genome was unable to replicate in these cells. Attempts to infect the Huh 7 cells with the chimera were more successful. Four days after incubation with 2 X 104 25 EBTr(A) tissue culture infectious doses (TCID) of the chimera, Huh 7 cells could be stained with antibody to NS3 as well as with antibody to HCV. Quantification of the number of infected cells indicated that the inoculum contained 10^3 TCID /ml for Huh 7 as compared to $10^5/\text{ml}$ 30 for EBTr(A) cells. Although the cells could be infected, the virus did not spread, suggesting that in Huh 7 cells , as in the MDBK and BT cells, virions either were not assembled or were not released from 35 cells. Most likely, the CP-7 virus could not provide the

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antibody but at a lower titer. Since the DNA vaccine expressed only the E2 glycoprotein, this protein must be involved in binding to Huh 7 cells. The plasma from chimp 1530 contained antibodies to the HCV envelope proteins as measured by ELISA or immunofluoresence microscopy but apparently, these were not neutralizing antibodies. Chimpanzee 1494 did not have demonstrable antiodies against the HCV glycoproteins so its failure to neutralize was not unexpected. Therefore, the chimera should be very useful for screening samples for neutralizing antibodies and discriminating between those that neutralize as compared to those that just bind.

Table 5

Neutralization of chimeric virus growth in Huh 7 cells¹

	Number of foci ²				
Virus dilution	Fetal Calf Serum (Boyt)	Anti-HCV HVR1	Anti-BVDV		
Undiluted	191	298	0		
Dilution (1:10)	23	43	0		

- 1. Huh 7 cells were used for infection but the virus had been grown in EBTr (A) cells.
- 2. Foci stained with chimp 1530 anti-HCV and visualized by immunofluoresence microscopy.

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glycoproteins were synthesized, it would be feasible to test purified chimeric virions as a candidate inactivated vaccine. Purified chimeric virions can be tested first in mice and if antibody to HCV is produced, the virions will be tested in chimpanzees to determine if the candidate vaccine is efficacious. The fact that virions grown in EBTr(A) cells were able to infect Huh 7 cells and were neutralized by some anti-HCV positive plasmas (Table 6) suggests that such chimeric viruses could be used to screen for neutralizing antibodies to HCV as well as to screen other cell lines for HCV receptors. The infectivity of the chimera proves the principle that HCV-BVDV chimeras can serve as a useful tool for studying the molecular biology of HCV. glycoprotein genes from the five other genotypes of HCV can be similarly inserted into the BVDV backbone in order to provide an assay for antibodies to each genotype. Additional chimeras are being constructed in which the core protein of BVDV is included so that only the glycoproteins of HCV are introduced. If BVDV core is critical for encapsidation of the RNA, it may be possible to generate chimeric viruses in the absence of It will also be revealing to determine if the HCV contribution to the chimera can be localized to either El or E2 alone. Such a chimera will be tested for its ability to infect EBTr(A) and Huh 7 cells. These studies will help determine the relative importance of El and E2 for infection of Huh 7 cells and may define any association with the BVDV glycoproteins. In addition, chimeras in which the BVDV nonstructural genes such as p7 or NS4B or NS5A are replaced with the corresponding genes of HCV may also be generated to

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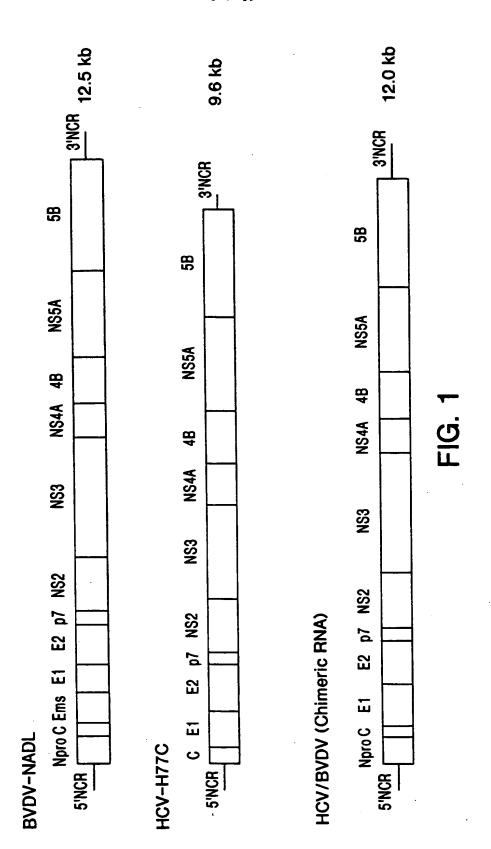
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-37**-**

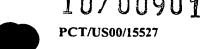
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has been replaced by the non-structural region of a hepatitis C virus genome.

- 8. The nucleic acid molecule of claim 7, wherein at least one gene from the non-structural region of the BVDV genome has been replaced by the corresponding gene from the non-structural region of a hepatitis C virus genome.
- 9. A DNA construct comprising the nucleic acid molecule of claims 1, 2 or 7.
 - $$10.\,$ An RNA transcript of the DNA construct of claim 9.
- 11. A polypeptide encoded by the nucleic acid15 molecule according to claim 1.
 - 12. A polypeptide encoded by the nucleic acid molecule according to claim 2.
- 13. The polypeptide according to claim 12, wherein said polypeptide is selected from the group consisting of E1, E2 or C.
 - 14. A host cell transfected with the DNA construct of claim 9.
- 25 15. A host cell transfected with the RNA transcript of claim 10.
- 16. A chimeric HCV-BVDV virus produced by
 transfecting a host cell with the DNA construct of claim
 30
 9.
 - 17. A chimeric HCV-BVDV virus produced by transfecting a host cell with the RNA transcript of claim 10.



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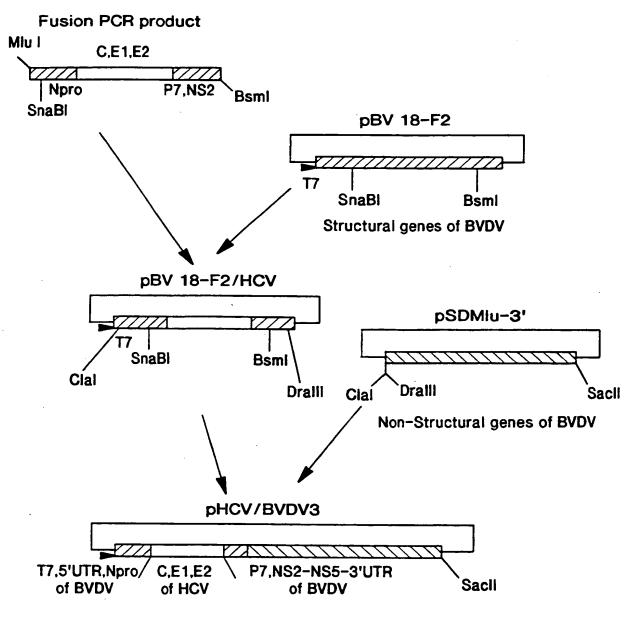


FIG. 2





H77C

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7.0	20				
1224567800			40	50	
1234307630	1234567890	1234567890	1234567890	1234567890	
	TGATGGGGC				50
	TCTTCACGCA				100
TGTCGTGTAB	CCTCCAGGAC		GGAGAGCA	TAGIGGICIG	150
CAMANACCOCI	GAGTACACCG	CAATICCAG	GACGACCGGG	TCCTTTCTTG	200
	CICAATGOOT				250
	GIGITGGGIC				300
	GIGOOOGG	AGGICIUGIA	GACCGIGCAC	CATGAGCAGG	350
	CTCAAAGAAA				400
	TTCCCGGGTG				450
	GGGCCCTAGA				500
	AACCTOGAGG				550
	AGGACCTGGG				600
	TIGCGGGIGG				650
	GGGGCCCCAC				700
	GATACCCTTA				750
TACCGCTCGT	CGGCGCCCT	CTTGGAGGCG	CIGCCAGGGC	CCTGGCGCAT	800
GGCCICCGGC	TICIGGAAGA	CCCCCTCAAC	TATGCAACAG	GGAACCTTCC	850
	TICICIAICT				900
	AGCCIACCAA				950
ACCAATGATT	GCCCIAACIC	GAGTATIGIG	TACGAGGGG	CCGATGCCAT	1000
CCTGCACACT	CCGGGGIGIG	TCCCTTCCGT	TCCCCAGGGT	AACGCCTCGA	1050
GIGIIGGI	GGCGGIGACC	CCCACGGIGG	CCACCAGGGA	CCCCAAACTC	1100
CCCACAACCC	AGCTTCGACG	TCATATCGAT	CIGCITGICG	GGAGCGCCAC	1150
CCICICCICG	GCCCTCTACG	TGGGGGACCT	GIGGGGGTCT	GICTITCTIG	1200
TIGGICAACT	GTTTACCTTC	TCTCCAGGC	CCCACTGGAC	GACGCAAGAC	1250
TGCAATTGIT	CIAICIAICC	CCCCATATA	ACCOGNICATO	GCATGGCATG	1300
GCATATGATG	ATGAACTGGT	CCCCTACGGC	AGOGITGGTG	GIAGCICAGC	1350
TGCTCCGGAT	CCCACAAGCC	ATCATGGACA	TGATCCCTGG	TECTCACTEG	1400
CCACTCCTCC	CGGGCATAGC	GIATTICICC	ATGGTGGGGA	ACTGGGGGAA	1450
GGICCIGGIA	GIGCIGCIGC	TATTIGCCCG	CCTCCACCCC	GAAACCCACG	1500
TCACCEGGGG	AAATGCCCGC	CGCACCACGG	CIGGGCTIGT	TEGICICETT	1550
ACACCAGGCG	CCAAGCAGAA	CATCCAACIG	ATCAACACCA	ACCCAGTIG	1600
	AGCACGGCCT				1650
GETTAGCAGG	CCICITCIAT	CAACACAAAT	TCAACTCTTC	AGGCTGTCCT	1700
CACACCTICC	CCACCIGCCG	ACCCTTACC	GATTTTGCCC	AGGGCTGGGG	1750
TCCTATCAGT	TATECCAACG	GAAGCGGCCT	CCACCAAACCC	CCCTACTCCT	1800
GCCACTACCC	TOCAAGACCT	TGTGGCATTG	TOCCCOCAAA	CACCETETET	1850
GCCCCGGTAT	ATTICCTTCAC	TCCCAGCCCC	टाव्हाव्हाव्ह	GAACGACCGA	1900

FIG. 3A

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H77C

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
			TGCAAATGAT		1950
			GCAATIGGIT		2000
			TGGGGAGGGC		2050
CATCGGAGGG	GIGGGCAACA	ACACCITGCT	CIGCCCACT	CATTCCTTCC	2100
			CCCCCCCCCC		2150
			AGGCTTTGGC		2200
			CATCLACCIG		2250
			CCCCCCCA		2300
			COGITECTEC		2350
			GACCCTGCCA		2400
			TEGACETECA		2450
			ATTAAGTGGG		2500
TCTCCTGTTC	CTTCTGCTTG	CAGACGCGCG	CCTCTCCTCC	TECTTETECA	2550
			CTTTGGAGAA		2600
			GICTIGIGT		2650
			TAGGIGGGIG		2 70 0
			TCCTCCTCCT		2750
			GIGGCCGCGT		2800
			TCTGTCGCCA		2850
GCTATATCAG	CTEGTECATE	TEGIESCITC	AGIATITICT	GACCAGAGIA	2900
GAAGCGCAAC	TGCACGIGIG	GETTCCCCCCC	CTCAACGTCC	GGGGGGGG	2950
			ACACCCGACC		3000
ACATCACCAA.	ACIACICCIG	CCCATCTTCG	GACCCCTTTG	GATTCTTCAA	3050
GCCAGTTTGC '	TIAAAGICCC	CIACMOGIG	CCCCTTCAAG	CCCTTCTCCC	3100
GATCTGCGCG (CTAGCGCGGA .	AGATAGCCCG	AGGICATTAC	GIGCAAAIGG	3150
			CCIAIGIGIA	TAACCATCIC	3200
				TEECCETEEC	3250
			GACCAAGCIC		3300
			TCAACGGCTT		3350
			CCACCCCACC		3400
			GGGTAGGCC		3450
CACCCTCCT	agggigiata i	ATCACCAGCC	TGACTGGGGG	GCACAAAAAC	3500
			ACTGCIACCC		3550
			TGTCTACCAC		3600
			TCATCCAGAT		3650
			CCICAAGGIT		3700
			TIACCIGGIC		3750
CCGATGICAT 1	iccciiccc	CCCCACCIG	ATACCAGGG	TAGCCIGCIT	3800

FIG. 3B



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H77C

10	20		40	50	
		1234567890			
		CITGAAAGGC			3850
		TGGGCCTATT			3900
		GACTITATOC			3950
		CACGGACAAC			4000
		ACCIGCATGC			4050
		TAGGCAGCCC			4100
		AACGCIGGGC		-	4150
		ATATCAGGAC			4200
CIGGCAGCCC	CATCACGIAC	TOTACCIACG	GCAAGITCCT	TECCEACEC	4250
GGGIGCICAG	GAGGIGCITA	TGACATAATA	ATTIGIGACG	AGTGCCACTC	4300
CACGGATGCC	ACATCCATCT	TGGGCATGGG	CACIGICCIT	GACCAAGCAG	4350
AGACTGCGGG	CCCCACACTG	GITGIGCICG	CCACTGCTAC	CCCICCCCCCCC	4400
TCCGTCACTG	TGTCCCATCC	TAACATCGAG	GAGGITGCIC	TGTCCACCAC	4450
CGCACACATC	CCCTTTTACG	GCAAGGCTAT	CCCCCTCCAG	GIGATCAACG	4500
GGGGAAGACA	TCTCATCTTC	TGCCACTCAA	AGAAGAAGTG	CCACCACCTC	4550
GCCGCGAAGC	TEGTESCATT	GGGCATCAAT	CCCTCCCCT	ACTACCGCGG	4600
TCTTGACGIG	TCTGTCATCC	CGACCAGCGG	CGATGITGIC	GICGIGICGA	4650
CCGATCCTCT	CATGACTGGC	TTTACCGGCG	ACTICGACIC	TGTGATAGAC	4700
TGCAACACGT	GIGICACICA	GACAGTCGAT	TTCAGCCTTG	ACCCIACCIT	4750
TACCATTGAG	ACAACCACGC	TCCCCCAGGA	TECTETCTCC	AGGACTCAAC	4800
GCCGGGGGCAG	GACTGGCAGG	GGGAAGCCAG	GCATCTATAG	ATTIGIGGCA	4850
CCGGGGGAGC	CCCCCTCCCCC	CATGITCGAC	TOGTOGTO	TCTGTGAGTG	4900
CIAIGACGCG	CCCIGICCIT	GGTATGAGCT	CACCCCCCC	GAGACTACAG	4950
TEAGGCEACG	AGCGIACAIG	AACACCCCGG	CCTTCCCT	GIGCCAGGAC	5000
CATCTIGAAT	TTTCCCACCC	CGICITIACG	GCCTCACTC	ATATAGATCC	5050
CCACTITITA	TCCCAGACAA	ACCAGAGTCG	GGAGAACTTT	CCTTACCTCG	5100
TAGCGIACCA .	AGCCACCGIG	TGCGCTAGGG	CTCAAGCCCC	TOCCCCATOG	5150
TOGGACCAGA	TGTGGAAGTG	TTTGATCCCC	CTTAAACCCA	CCCTCCATGG	5200
GCCAACACCC	CIGCIATACA	GACTGGGGGC	TGTTCAGAAT	GAAGTCACCC	5250
TGACGCACCC	AATCACCAAA	TACATCATGA	CATCCATGIC	GGCGACCTG	5300
CACCTCCTCA	CGAGCACCIG	GGIGCICGIT	COCCESSION CO.	TESCICCICT	5350
GGCCGCGIAT	TGCCTGTCAA	CAGGCTGCGT	GGTCATAGTG	CCCACCATCG	5400
TCTTGTCCCC	GAAGCCCGGCA	ATTATACCIG	ACAGGGAGGT	TCTCTACCAG	5450
CACTTCCATG	AGATOGAAGA	GIGCICICAG	CACTTACOGT	ACATOGAGOA	5500
ACCCATGATG	CTCGCTGAGC	AGTTCAAGCA	GAAGGCCCTC	GCCICCIGC	5550
AGACCGCGTC	CCGCCATGCA	GAGGITATCA	cccrecrer	CCAGACCAAC	5600
TGGCAGAAAC	TCGAGGICTT	TIGGGGAAG	CACATGTGGA	ATTICATCAG	5650
TGGGATACAA	TACTIGGGG	CCCTGTCAAC	CTCCTCGT	AACCCCCCCA	5700

FIG. 3C SUBSTITUTE SHEET (RULE26)



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H77C

10	20	30	40	<u> </u>	
	_		1234567890	50 1234567890	
			TCACCAGCCC		5750
			GGGIGGGIGG		5800
			GGGIGCIGGC		5850
			TCCTCGTGGA		5900
			GIAGCATICA		5950
			CAATCIGCIG		6000
TCTCCCCTCC	AGCCCTTGTA	GICEGIGIGE	TCTGCGCAGC	AATACIGOGC	6050
CCCCACCTTC	CCCCCCCCA	GGGGGCAGTG	CAATGGATGA	ACCGCTAAT	6100
AGCCTTCGCC	TCCCGGGGGA	ACCATGITIC	CCCCACGCAC	TACGICCOCC	6150
AGAGCGATGC	AGCCGCCCCC	GICACIGOCA	TACTCAGCAG	CCICACIGIA	6200
ACCCAGCTCC	TGAGGCGACT	GCATCAGTGG	ATAAGCTCCG	AGIGIACCAC	6250
TCCATGCTCC	GELLCCLGGC	TAAGGGACAT	CIGGGACIGG	ATATGOGAGG	6300
TECTGACCGA	CTTTAAGACC	TGGCTGAAAG	CCAAGCICAT	GCCACAACIG	6350
CCTGGGATTC	CCTTIGIGIC	CTGCCAGCGC	GGGTATAGGG	GGGTCTGGGG	6400
AGGAGACGGC	ATTATGCACA	CTCGCTGCCA	CIGIGGAGCT	GAGATCACTG	6900
GACATGTCAA	AAACGGGACG	ATGAGGATCG	TOGGTOCTAG	GACCIGCAGG	6950
AACATGTGGA	GIGGGACGIT	CCCCATTAAC	GCCTACACCA	CGGGCCCCIG	6550
TACTOCCCTT	ASSOCIOSOS	ACTATAAGIT	CCCCCICICC	AGGGIGICIG	6600
CAGAGGAATA	CCTCCACATA	AGGCGGGTGG	GGGACTTCCA	CIACGIATOG	6650
GGIAIGACIA	CIGACAAICI	TAAATGCCCG	TCCCAGATCC	CATOGCOGA	670 0
ATTITICACA	GAATTGGACG	GGGIGGGCCT	ACACAGGTTT	CCCCCCTT	6750
GCAAGCCCTT	242222222	GAGGIATCAT	TCAGAGIAGG	ACTOCACGAG	6800
TACCCCGTCG	CCICCCAATT	ACCITICCGAG	CCCGAACCGG	ACGIAGCOGT	6850
GITGACGICC	ATGCTCACTG	ATCCCTCCCA	TATAACAGCA	CAGGGGGGG	6900
GGAGAAGGIT	CCCACACACCC	TCACCCCCTT	CTATEGCCAG	CICCICGGCT	6950
AGCCAGCIGI	CCGCTCCATC	TCTCAAGGCA	ACTIGCACCG	CCAACCATGA	7000
CICCCCIGAC	CCCCACCTCA	TAGAGGCTAA	CCICCIGIGG	AGGCAGGAGA	7050
TGGGCGGCAA	CATCACCAGG	GIIGAGICAG	AGAACAAAGT	GGIGATICIG	7100
GACTCCTTCG	ATCCCCTTCT	GGCACAGGAG	CATGAGGGGG	AGGICICOGT	7150
			ATTOGCCOGG		7200
				GIGGAAAAAG	
			TGCCCCCTAC		7300
			COSTACOSTG		7350
			TIGCCACCAA		7400
				CATCCICIGA	7450
			CCACGITGAG		7500 7550
-			ATCCGGATCT		7550 7600
TCATEGICGA	CGGICAGIAG	TGGGGGAC	ACCEAAGAIG	TOGIGIGOIG	7600

FIG. 3D

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H77C

			·		
10	20		40	50	
	1234567890				
	TATTCCTGGA				7650
	ACTGCCCATC				7700
	TGEATTCCAC				7750
	TTTGACAGAC			-	7800
	GGTCAAAGCA				7850
TCCGTAGAGG	AAGCTTGCAG	CCIGACGCCC	CCACATTCAG	AACOTAAACO	7900
	GGGGCAAAAG				7950
	CICCEIGICS				8000
	CCATCATGGC				8050
	CGIAAGCCAG	*			8100
	CGAGAAGAIG				8150
	TEEGAAGCTC				8200
GGTTGAATTC	CTCGTGCAAG	CGIGGAAGIC	CAAGAAGACC	CCCATGGGGT	8250
TCTCCTATGA	TACCCCCTGT	TTTGACTCCA	CAGICACIGA	GAGCGACATC	8300
CGTACGGAGG	AGGCAATITA	CCAAIGIIGI	GACCIGGACC	CCCAAGCCCG	8350
CGTGGCCATC	AAGTCCCTCA	CIGAGAGGCT	TIAIGIIGGG	GGCCCTCTTA	8400
CCAATTCAAG	GGGGGAAAAC	TGCGGCTACC	GCAGGTGCCG	CCCCAGCCCC	8450
GIACIGACAA	CTAGCIGIGG	TAACACCCTC	ACTIGCIACA	TCAAGGCCCG	8500
GGCAGCCIGI	CGAGCCGCAG	GGCTCCAGGA	CIGCACCATG	CICCIGIGIG	8550
CCCACGACTT	AGICGITAIC	TGTGAAAGTG	CCCCCCCA	GCAGCACGCC	8600
GCGAGCCTGA	GAGCCTTCAC	GGAGGCTATG	ACCAGGIACT	accentance	8650
CGGGGACCCC	CCACAACCAG	AATACGACTT	GGAGCTTATA	ACATCATGCT	8 70 0
	GTCAGTCGCC				8750
CTTACCCGTG	ACCCIACAAC	CCCCTCCCC	AGAGCCGCGT	GGGAGACAGC	8800
AAGACACACT	CCAGICAAIT	CCTGGCTAGG	CAACATAATC	AIGITIGCCC	8850
CCACACTGTG	GGCGAGGAIG	ATACIGATGA	CCCATTICTT	TAGOGICCIC	8900
	ATCAGCTTGA				8950
	ATAGAACCAC				9000
	CCCATTTTCA				9050
AGGGTGGCCG	CATGCCTCAG	AAAAÇITIGGG	GICCCCCCT	TGCGAGCTTG	9100
GAGACACCGG	GCCCGGAGCG	TCCGCCCTAG	CCTTCTGTCC	AGAGGAGGCA	9150
GGGCTGCCAT	ATGTGGCAAG	TACCICITCA	ACTGGGCAGT	AAGAACAAAG	9200
CICAAACICA	CTCCAATAGC	GCCCCCIGCC	CGGCTGGACT	TGICCGGITG	9250
	GGCTACAGCG				9300
	CIGGITCIGG				9350
	TCCTCCCCAA				9400
	TITCCIGITI				9450
TTTTTTTCTT	TECTTICETT	CITITITICC	TITCITITIC	CCTTCTTEAA	9500

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H77C

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
TEGTESCICC					9550
GCCGCATGAC	TCCAGAGAGT	GCTGATACTG	CCCICICICC	AGATCATGT	9599

FIG. 3F



PCT/US00/15527

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H77C

10	20	,30	40		
		30 1234567890	40 1234567890	50 1234567890	
MSINPKPORK	TKRNINRRPQ	DVKFPGGGQI	VGGVYLLPRR	GPRI GVRATR	50
KISERSOPRG	RROPIPKARR	PEGRIWAQPG	YPWPLYGNEG	CEVEDANE I SP	100
RGSRPSWGPT	DPRRRSRNLG	KVIDILIOGF	ADLMGYIPLV	GAPIGGAARA	150
LAHGVRVLED	GVNYATGNLP	GCSFSIFLLA	LLSCLIVPAS	AYOVRNS9GI.	200
YHVINDCHNS	SIVYEAADAI	LHIPGCVPCV	REGNASROW	AVIPIVATRD	250
CKLPTTQLRR	HIDLLVGSAT	LCSALYVEDL	CGSVFLVGQL	FIFSPRRHWI	300
TODONOSIYP	GHTGHRMAW	IMMNWSPIA	ALVVAOLLRI	POATMIMITAG	350
AHWGVLAGIA	YFSMVGWAK	VLVVLLLFAG	VDAEIHVIGG	NAGRITAGIV	400
GLLTPGAKQN	IQLININGSW	HINSTALNON	ESLNIGWLAG	LFYCHKENSS	450
GCPERLASCR	RLIDFAQGWG	PISYANGSGL	DERPYCWHYP	PRPOGIVPAK	500
SVCGPVYCFT	PSPVVVGTTD	RSGAPTYSWG	ANDIDVFVLN	NIRPPLOWF	550
GCTWMNSTGF	TKVCGAPPCV	IGGVGNNILL	CPIDCFRKHP	EATYSRCGSG	600
PWITPROMVD	YPYRLWHYPC	TINYTIFKVR	MYVGGVEHRL	EAACIWIRGE	650
RCDLEDRDRS	ELSPLLLSTT	QWQVLPCSFT	TLPALSIGLI	HLHQNIVDVO	700
YLYGVGSSIA	SWAIKWEYVV	LLFLLLADAR	VCSCLWMLL	ISOAFAALEN	750
LVIINAASLA (GIHGLVSFLV	FFCFAWYLKG	RWPGAVYAL	YGMWPLLLLL	800
LALPQRAYAL :	DIEVAASCGG	VVLVGLMALT	LSPYYKRYIS	WMWLQYFL	850
TRVEAQLHW '	VPPLNVRGGR	DAVILLMCVV	HPTLVFDITK	LLLAIFGPLW	900
ILQASLLKVP :	YFVRVQGLLR	ICALARKIAG	CHYVQMAIIK	LGALTGTYVY	950
NHLTPLRDWA 1	HNGLRDLAVA '	VEPVVFSRME	TKLITWGADT	AACGDIINGL	1000
PVSARRGQEI I	LLGPADGMVS :	KOWRLLAPIT .	AYAQQTRGLL	CCITTSLICER	1050
DKNOVEGEVQ :	IVSTATQIFL .	ATCINGVCWT	VYHGAGIRII	ASPKGPVIQM	1100
ALINADODING A	WPAPQGSRSL'	TPCTCGSSDL	YLVIRHADVI	PVRRRGDSRG	1150
		CPAGHAVGLF :			1200
LGTIMRSPVF :	IDNSSPPAVP (QSFQVAHLHA	PIGSGKSIKV	PAAYAAQGYK	1250
VLVLNPSVAA 1	ILGFGAYMSK I	AHGVDRNIRI	GVRITTIGSP	ITYSIYGKFL	1300
ADGGCSGGAY I					1350
PPGSVIVSHP 1					1400
DELAAKLVAL (1450
ATDOMICATÓ J	IVDFSLDPIF :	TIETTILPQD A	AVSRIQRRGR	TGREKPGIYR	1500
FVAPGERPSG N					1550
CODHLEFWEG \	/FIGLTHIDA I	HFLSQIKQSG :	ENFPYLVAYQ	ATVCARAQAP	1600
PPSWDQMWKC I	IRLKPILHG 1	PIPLLYRLGA '	VQVEVILIHP	TIKYIMIOMS	1650
ADLEVVISIW \	/LVGGVLAAL /	AAYCLSIGCV '	VIVGRIVLSG	KPAIIPDREV	1.700
LYQEFDEMEE (SCHLPYIEQ (AMIAEQFKQ	KALGLIQIAS	RHAEVITPAV	1750
QINWQKLEVF V	WANTEMNETS (SIQYLAGLST :	LPGNPAIASL	MAFTAAVISP	1800
LTTGQTLLFN 1	LLGAWAAQL X	AAFGAATAFV (GAGLAGAAIG	SVGLCKVLVD	1850
ILAGYGAGVA (*ALVAFKIMS (GEVPSTEDLV 1	NLLPAILSPG	ALVVGVVCAA	1900

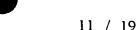
FIG. 3G SUBSTITUTE SHEET (RULE**26**) 10 / 19



H77C

					
10	20	30	40	50	
<u>1234567890</u>	<u> 1234567890</u>	<u> 1234567890</u>	1234567890	1234567890	
ILRRHVGPGE	GAVQWMNRLI	AFASROVHVS	PIHYVPESDA	AARVIAILSS	1950
LIVIQLLRRL	HOWISSECTT	PCSGSWLRDI	WDWICEVLSD	FKIWLKAKLM	2000
				NGIMRIVGPR	2050
				VEIRRVGDFH	2100
AASCALLIDAL	KCPCQIPSPE	FFTELDGVRL	HRFAPPCKPL	LREEVSFRVG	2150
LHEYPVGSQL	PCEPEPDVAV	LTSMLTDPSH	ITAEAAGRRL	ARGSPPSMAS	2200
SSASQLSAPS	LKATCIANHD	SPDAELIEAN	LLWRQEMEGN	TIRVESENKV	2250
VILDSFDPLV					2300
WKKPDYEPPV					2350
SFGSSSTSGI					2400
SDGSWSTVSS					2450
LRHHNLVYST					2500
NLLSVEEACS :	LIPPHSAKSK	FGYGAKDVRC	HARKAVAHIN	SVWKDLLEDS	2550
VIPIDITIMA :	KNEVFCVQPE	KGGRKPARLI	VFPDLGVRVC	EKMALYDVVS	2600
KLPLAVMGSS '	YGFQYSPGQR	VEFLVQAWKS	KKIPMGFSYD	TRCFDSTVIE	2650
SDIRTEEATY (QCCDLDPQAR	VAIKSLIERL	YVGGPLINSR	GENCGYRROR	2700
ASGVLTTSCG 1					2750
EDAASLRAFT I					2800
VYYLTRDPTT I					2850
SVLIARDQLE (2900
EINRVAACLR H					2950
RIKLKLTPIA A					3000
AGVGIYLLPN F					3011

FIG. 3H





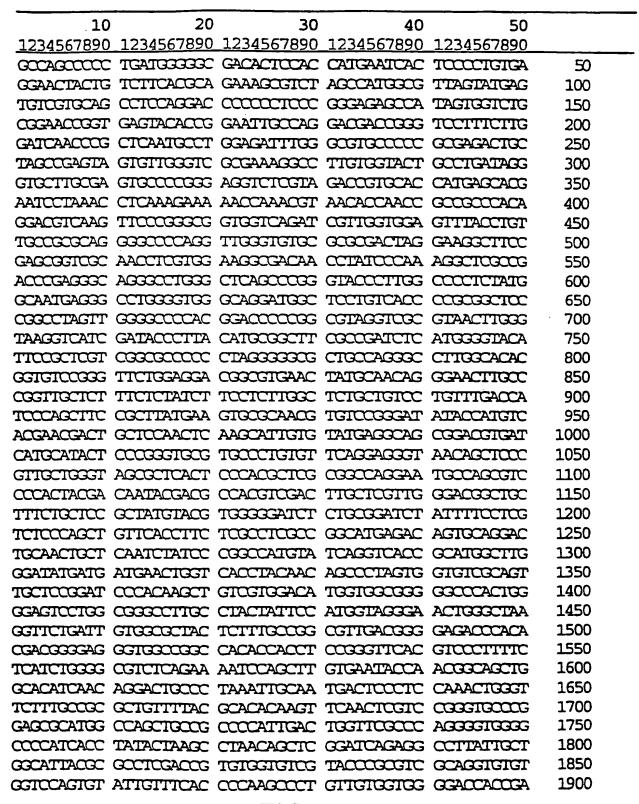


FIG. 4A



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			GCAACIGGIT		2000
			TECCEGAGGIC		2050
			CIGCCCACG		2100
			GIGGCIGGG		2150
			AGGCTTTGGC		2200
			CATGIATGIG		2250
AGCACAGGCT					2300
TTGGAGGACA					2350
AGAGIGGCAG					2400
CIGGITIGAT					2450
GGTGTAGGGT					2500
GITGCITTIC					2550
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GITCITCIGC	GCCGCCTGGT	ACATTAAGGG	CAGGCTGGCT	CIGGGGGG	2700
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TGTTTCTCAC '	TAGGCTCATA	TEGTEGTTAC	AATACTTTAT	CACCAGAGGC	2900
GAGGCGCACA '					2950
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ACATCACCAA A					3050
GCTGGCATAA (3100
TGCATGCATG !					3150
TCTTCATGAA (3CTGGGGGGG	CIGACAGGIA	CGTACGITIA	TAACCATCIT	3200
ACCCCACTGC (GGACTGGGC	CCACGCGGGC	CIACGAGACC	TIGOGGIGGC	3250
GGIAGAGCCC (FICGICITCI	CCGCCATGGA	GACCAAGGIC	ATCACCTGGG	3300
GAGCAGACAC (3350
GCCCGAAGGG (GAAGGAGAT.	ATTTTTGGGA	CCGGCTGATA	GICICGAAGG	3400
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GGGGCGIACT T					3500
CAGGICGAAG (EGAGGITCA .	AGIGGITICI	ACCGCAACAC	AATCTTTCCT	3550
GGGGACCTGC A					3600
CGAAGACCCT A					3650
GTAGACCTGG A					3700
GACACCATGC A					3750
CIGATGICAT 1	icceriecec (CGGCGAGGCG	ACAGCAGGGG	AAGICIACIC	3800
			. —		

FIG. 4B SUBSTITUTE SHEET (RULE26) 13 / 19

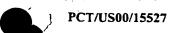


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		GACTICATAC			3950
ACCATGCGGT		CACAGACAAC			4000
GCAGACATTC		ATCTGCACGC			4050
		TATGCAGCCC			4100
			TITIGGGGGGT	_ _ _ _	4150
		ACATCAGAAC			4200
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GCIGIICIG		TGACATCATA		· - - -	4300
		TEGECATOGG			4350
		GICGICCICG			4400
		CAATATCGAG			4450
		GCAAAGCCAT		GCCATCAAGG	4500
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GCCGCAAAGC	TGACAGGCCT	CGGACTGAAC			4600
		CCCTATCCG		GICGIGGCAA	4650
CAGACGCTCT	AATGACGGGT	TTCACCGGGG	ATTTTGACTC	AGIGATOGAC	470 0
TGCAATACAT	GIGICACCCA	GACAGTOGAC	TTCAGCTTGG	ATCCCACCIT	4750
CACCATTGAG	ACGACGACCG	TGCCCCAAGA	CCCCCTCTCCC	CGCTCGCAAC	4800
CCCCACCTAC	AACTGGCAGG	GGTAGGAGTG	GCATCTACAG	GITIGICACT	4850
CCAGGAGAAC	GGCCTCGGG	CATGITCGAT	TCTTCGGTCC	TGIGIGAGIG	4900
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CCACTTCCTG	TCCCAGACTA	AACAGGCAGG	AGACAACITT	CCTTACCTGG	5100
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GCCAACACCC	CICCIGIATA	GGCTAGGAGC	CGICCAAAAT	GAGGICATOC	5250
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TCTTGTCCGG	GAAGCCAGCT	GICGITCCCG	ACAGGGAAGT	CCTCTACCAG	5450
GAGTICGAIG .	AGATGGAAGA	GIGIGCCICA	CAACITCCIT	ACATCGAGCA	5500
		AATTCAAGCA			5550
		GAGGCTGCTG			5600
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FIG. 4C



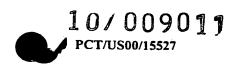


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	CAGCATAGGC				5900	
	CAGGGGIAGC				5950	
	CCCTCCACCG				6000	
	TECCCIGGIC				6050	
	GCCCCGGGAGA				6100	
	TCGCGGGGIA				6150	
	TGCAGCACGT				6200	
	TGAAGOGGCT				6250	
	GCICCIGCC				6300	
	CITCAAGACC				6350	
	CITICCIGIC				6400	
	ATCATGCAAA				6450	
	AAACGGTTCC				6500	
	ACGGAACGIT				6550	
	CCGGCGCCA				6600	
	CGIGGAGGIT				6650	
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GCAAACCICT '					6800	
TACTIGGICG (6850	
GCTTACTTCC 2					6900	
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AGCCAGTIGT (7000	
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TGGGCGGAAA (7100	
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TATEGGCACG (7250	
CCGGACTACG					7300	
GGCTCCTCCA A					7350	
AATCCAATGT (7400	
AGCTCCGGAT (7450	
CCIGGCCICC (7500	
CCATGCCCCC (7550	
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FIG. 4D SUBSTITUTE SHEET (RULE26)



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AACATGGTCT	ACCCCACAAC	ATCCCGCAGC	GCAAGCCTCC	GGCAGAAGAA	7750
GGTCACCTTT	CACACATICC	AAGTOCTOGA	TGATCATTAC	CCCCACCIAC	7800
TCAAGGAGAT	CAACCCCAAC	COCTICCACAG	TTAAGGCTAA	GCTTCTATCT	7850
ATAGAGGAGG	CCIGCAAGCI	GACCOCCCA	CATTOGGCCA	TTAAACOTAA	7900
TEGETATEGG	GCAAAGGACG	TCCGGAACCT	ATCCAGCAGG	GCCGTTAACC	7950
ACATOGGCTC	CGIGIGGGAG	CACTICCICG	AAGACACTGA	AACACCAATT	8000
GACACCACCA	TCATGGCAAA	AAGIGAGGTT	TTCTGCGTCC	AACCAGAGAA	8050
GGCAGGCCGC	AAGCCAGCTC	GCCTTATCGT	ATTCCCAGAC	CIGGGAGITC	8100
GIGIAIGCGA	GAAGATGGCC	CTTTACGACG	TEGTCTCCAC	CCTTCCTCAG	8150
CCCGTGATCG	GCTCCTCATA	CCCATTICAA	TACTCCCCCA	AGCAGCGGGT	8200
CGAGITCCIG	GIGAATACCT	GGAAATCAAA	GAAATGCCCT	ATGGGCTTCT	8250
CATATGACAC	CCCCTGTTTT	GACTCAACGG	TCACTGAGAG	TGACATTCGT	8300
GITGAGGAGT	CAATTIACCA	ATGITGIGAC	TTGGCCCCCG	AGGCCAGACA	8350
GGCCATAAGG	TCGCTCACAG	AGCGGCITIA	CATCGGGGGT	CCCCTGACTA	8400
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CTGACGACTA	GCTGCGGTAA	TACCCTCACA	TGTTACTTGA	AGGCCACTGC	8500
AGCCTGTCGA	GCTGCAAAGC	TOCAGGACIG	CACGATGCTC	GTGAACGGAG	8550
ACGACCTIGT	CGITATCIGI	GAAAGCGCGG	GAACCCAGGA	GCATGCGGCG	8600
GCCCTACGAG	CCTTCACGGA	GGCIAIGACT	AGGIATICCG	cccccccccc	8650
GGATCCGCCC		ACGACCTGGA	GCTGATAACA	TCAIGITCCT	8700
CCAATGIGIC	AGTCGCGCAC	GATGCATCTG	GCAAAAGGGT	ATACIACCIC	8750
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			CIGGACIIGI		9250
			TCACAGCCTG		9300
			TACTITCIGI		9350
			AGCTAACCAC		9400
			TITTTTTTT		9450
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FIG. 4E

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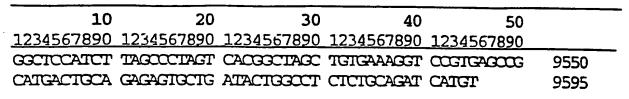
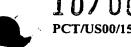


FIG. 4F



					
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		GCSFSIFLLA			200
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ASVPITTIRR	HVDLLVGTAA	FCSAMYVCDL	CGSIFLVSQL	FIFSPRRHET	300
VQDONCSIYP	GHVSGHRMAW	IMMNWSPIT	ALVVSQLLRI	PQAVVIMVAG	350
ALDAIVOWHA	AXZMAZMAK	VLIVALLFAG	VDGEIHTTGR	VAGHITSGFT	400
SLFSSGASQK	IQLVNINGSW	HINRIALNON	DSLQIGFFAA	LFYAHKFNSS	450
GCPERMASCR	PIDWFAQGWG	PITYTKPNSS	DORPYCWHYA	PRPOGVVPAS	500
QVCGPVYCFT	PSPVVVGTTD	RSGVPTYSWG	ENEIDVMLIN	NIRPPOGNMF	550
CCIWMNSTGF	TKTCGGPPCN	IGGVGNRILI	CPIDCFRKHP	EATYTKCGSG	600
PWLTPRCLVD	YPYRLWHYPC	TLNFSIFKVR	MYVGGVEHRL	NAACNWIRGE	650
RONLEDRORS	ELSPLLLSTT	EWQILPCAFT	TLPALSTGLI	HTHÖNINDAÖ	70 0
YLYGVGSAFV	SFAIKWEYIL	LLFLLLADAR	VCACLWMLL	IAQAEAALEN	750
LVVLNAASVA	GAHGILSFLV	FFCAAWYIKG	RLAPGAAYAF	YGWPLLLLL	800
		AVLVGLVFLT		-	850
TRAEAHMOW	VPPLNVRGGR	DAITLLTCAV	HPELIFDITK	LLLATIGPIM	900
_		ACMLVRKVAG	-		950
NHLTPLRDWA	HAGLRDLAVA	VEPVVFSAME	TKVITWGADI	AACCOILLCL	1000
PVSARRGKEI	FLGPADSLEG	QGWRLLAPIT	AYSQQIRGVL	CCITISLICER	1050
DKNOVEGEVQ	WSTATQSFL	ATCINGVCWT	VYHGAGSKTL	AGPKGPITQM	1100
YINVDLDLVG	WQAPPGARSM	TPCSCGSSDL	YLVIRHADVI	PVRRRGDSRG	1150
SLLSPRPVSY	LKGSSGGPLL	CPSCHVVGVF	RAAVCTRGVA	KAVDFIPVES	1200
METTMRSPVF	TINSTPPAVP	QTFQVAHLHA	PIGSGKSIKV	PAAYAAQGYK	1250
VLVLNPSVAA	TLGFGAYMSK	AHGIDPNIRI	GVRTTTTGGS	TTYSTYCKFL	1300
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		GEIPFYGKAI			1400
DELAAKLIGL	GLNAVAYYRG	LDVSVIPPIG	DVVVVATDAL	MIGFIGDEDS	1450
		TIETTIVPQD			1500
		YDAGCAWYEL			1550
		HFLSQIKQAG	_		1600
- 		PTPLLYRLGA	-		1650
			=	KPAVVPDREV	1700
	_	GMOLYEOLKÓ			1750
		GIQYLAGLST			1800
- -	_			SIGLGKVLVD	1850
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FIG. 4G

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PRLPGVPFLS	CORGYKGWR	COCIMOTICE	CCAQIACHVK	NGSMRIVGPR	2050
TCSNIWHGIF	PINAYTIGPC	TPSPAPNYSR	ALWRVAAEEY	VEVIRVGDFH	2100
MILIDIM	KCPCQVPAPE	FFTEVDGVRL	HRYAPACKPL	LREDVIFQVG	2150
TWÖATAGGÖT	PCEPEPDVIV	LISMLIDPSH	ITAETAKRRL	ARGSPPSLAS	2200
SSASQLSAPS	LKATCITHHD	SPDADLIFAN	LLWRQEMEGN	ITRVESENKV	2250
VILDSFEPLH	AEGDEREISV	AAEILRKSRK	FPSALPIWAR	PDYNPPLLES	2300
			RIVVLIESW		2350
TFGSSGSSAV	DSGIATALPD	LASDDCEKGS	DVESYSSMPP	LEGERGOPDL	2400
SDGSWSIVSE	EASEDVVCCS	MSYTWICALI	TPCAAEESKL	PINPLSNSLL	2450
RHHMVYATT	SRSASLRQKK	VIFDRLQVLD	DHYRDVLKEM	KAKASTVKAK	2500
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FIG. 4H

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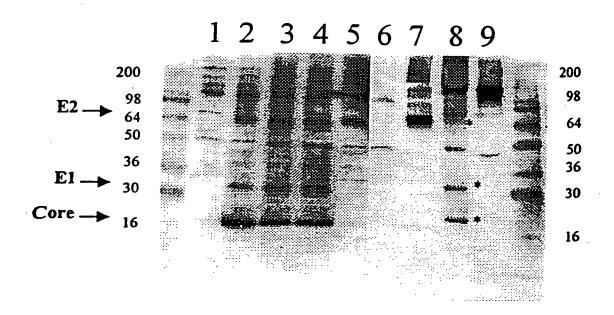


FIG. 5

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WO 00/75352

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tagetgggge eccaeagace eccggegtag gtegegeaat ttgggtaagg teategatae 1260
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- Lys Arg Gly Asp Cys Arg Ser Gly Asn Ser Arg Gly Pro Val Ser Gly 65 70 75 80
- Ile Tyr Leu Lys Pro Gly Pro Leu Phe Tyr Gln Asp Tyr Lys Gly Pro 85 90 95
- Val Tyr His Arg Ala Pro Leu Glu Leu Phe Glu Glu Gly Ser Met Cys
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- Glu Thr Thr Lys Arg Ile Gly Arg Val Thr Gly Ser Asp Gly Lys Leu 115 120 125
- Tyr His Ile Tyr Val Cys Ile Asp Gly Cys Ile Ile Ile Lys Ser Ala 130 135 140
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- Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr 485 490 495
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- Ala Ile Gln Tyr Gly Ser Gly Glu Val Val Met Met Gly Asn Leu Leu 915 920 925
- Thr His Asn Asn Ile Glu Val Val Thr Tyr Phe Leu Leu Leu Tyr Leu 930 935 940
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- Glu Ile Leu Asn Asn Leu Leu Ile Ser Glu Asp Leu Pro Ala Ala Val 2100 2105 2110
- Lys Asn Ile Met Ala Arg Thr Asp His Pro Glu Pro Ile Gln Leu Ala 2115 2120 2125
- Tyr Asn Ser Tyr Glu Val Gln Val Pro Val Leu Phe Pro Lys Ile Arg 2130 2135 2140
- Asn Gly Glu Val Thr Asp Thr Tyr Glu Asn Tyr Ser Phe Leu Asn Ala 2145 2150 2155 2160
- Arg Lys Leu Gly Glu Asp Val Pro Val Tyr Ile Tyr Ala Thr Glu Asp 2165 2170 2175
- Glu Asp Leu Ala Val Asp Leu Leu Gly Leu Asp Trp Pro Asp Pro Gly
 2180 2185 2190
- Asn Gln Gln Val Val Glu Thr Gly Lys Ala Leu Lys Gln Val Thr Gly
 2195 2200 2205
- Leu Ser Ser Ala Glu Asn Ala Leu Leu Val Ala Leu Phe Gly Tyr Val 2210 2215 2220
- Gly Tyr Gln Ala Leu Ser Lys Arg His Val Pro Met Ile Thr Asp Ile 2225 2230 2235 2240
- Tyr Thr Ile Glu Asp Gln Arg Leu Glu Asp Thr Thr His Leu Gln Tyr
 2245 2250 2255
- Ala Pro Asn Ala Ile Lys Thr Asp Gly Thr Glu Thr Glu Leu Lys Glu 2260 2265 2270
- Leu Ala Ser Gly Asp Val Glu Lys Ile Met Gly Ala Ile Ser Asp Tyr 2275. 2280 2285
- Ala Ala Gly Gly Leu Glu Phe Val Lys Ser Gln Ala Glu Lys Ile Lys 2290 2295 2300
- Thr Ala Pro Leu Phe Lys Glu Asn Ala Glu Ala Ala Lys Gly Tyr Val 2305 2310 2315 2320



- Gln Lys Phe Ile Asp Ser Leu Ile Glu Asn Lys Glu Glu Ile Ile Arg 2325 2330 2335
- Tyr Gly Leu Trp Gly Thr His Thr Ala Leu Tyr Lys Ser Ile Ala Ala 2340 2345 2350
- Arg Leu Gly His Glu Thr Ala Phe Ala Thr Leu Val Leu Lys Trp Leu 2355 2360 2365
- Ala Phe Gly Glu Ser Val Ser Asp His Val Lys Gln Ala Ala Val 2370 2375 2380
- Asp Leu Val Val Tyr Tyr Val Met Asn Lys Pro Ser Phe Pro Gly Asp 2385 2390 2395 2400
- Ser Glu Thr Gln Glu Gly Arg Arg Phe Val Ala Ser Leu Phe Ile 2405 2410 2415
- Ser Ala Leu Ala Thr Tyr Thr Tyr Lys Thr Trp Asn Tyr His Asn Leu 2420 2425 2430
- Ser Lys Val Val Glu Pro Ala Leu Ala Tyr Leu Pro Tyr Ala Thr Ser 2435 2440 2445
- Ala Leu Lys Met Phe Thr Pro Thr Arg Leu Glu Ser Val Val Ile Leu 2450 2455 2460
- Ser Thr Thr Ile Tyr Lys Thr Tyr Leu Ser Ile Arg Lys Gly Lys Ser 2465 2470 2475 2480
- Asp Gly Leu Leu Gly Thr Gly Ile Ser Ala Ala Met Glu Ile Leu Ser 2485 2490 2495
- Gln Asn Pro Val Ser Val Gly Ile Ser Val Met Leu Gly Val Gly Ala 2500 2505 2510
- Ile Ala Ala His Asn Ala Ile Glu Ser Ser Glu Gln Lys Arg Thr Leu 2515 2520 2525
- Leu Met Lys Val Phe Val Lys Asn Phe Leu Asp Gln Ala Ala Thr Asp 2530 2535 2540
- Glu Leu Val Lys Glu Asn Pro Glu Lys Ile Ile Met Ala Leu Phe Glu 2545 2550 2555 2560
- Ala Val Gln Thr Ile Gly Asn Pro Leu Arg Leu Ile Tyr His Leu Tyr
 2565 2570 2575



- Gly Val Tyr Tyr Lys Gly Trp Glu Ala Lys Glu Leu Ser Glu Arg Thr 2580 2585 2590
- Ala Gly Arg Asn Leu Phe Thr Leu Ile Met Phe Glu Ala Phe Glu Leu 2595 2600 2605
- Leu Gly Met Asp Ser Gln Gly Lys Ile Arg Asn Leu Ser Gly Asn Tyr 2610 2615 2620
- Ile Leu Asp Leu Ile Tyr Gly Leu His Lys Gln Ile Asn Arg Gly Leu 2625 2630 2635 2640
- Lys Lys Met Val Leu Gly Trp Ala Pro Ala Pro Phe Ser Cys Asp Trp
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- Thr Pro Ser Asp Glu Arg Ile Arg Leu Pro Thr Asp Asn Tyr Leu Arg 2660 2665 2670
- Val Glu Thr Arg Cys Pro Cys Gly Tyr Glu Met Lys Ala Phe Lys Asn 2675 2680 2685
- Val Gly Gly Lys Leu Thr Lys Val Glu Glu Ser Gly Pro Phe Leu Cys 2690 2695 2700
- Arg Asn Arg Pro Gly Arg Gly Pro Val Asn Tyr Arg Val Thr Lys Tyr 2705 2710 2715 2720
- Tyr Asp Asp Asn Leu Arg Glu Ile Lys Pro Val Ala Lys Leu Glu Gly
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- Gln Val Glu His Tyr Tyr Lys Gly Val Thr Ala Lys Ile Asp Tyr Ser 2740 2745 2750
- Lys Gly Lys Met Leu Leu Ala Thr Asp Lys Trp Glu Val Glu His Gly 2755 2760 2765
- Val Ile Thr Arg Leu Ala Lys Arg Tyr Thr Gly Val Gly Phe Asn Gly 2770 2775 2780
- Ala Tyr Leu Gly Asp Glu Pro Asn His Arg Ala Leu Val Glu Arg Asp 2785 2790 2795 2800
- Cys Ala Thr Ile Thr Lys Asn Thr Val Gln Phe Leu Lys Met Lys Lys 2805 2810 2815
- Gly Cys Ala Phe Thr Tyr Asp Leu Thr Ile Ser Asn Leu Thr Arg Leu 2820 2825 2830



- Ile Glu Leu Val His Arg Asn Asn Leu Glu Glu Lys Glu Ile Pro Thr
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- Ala Thr Val Thr Trp Leu Ala Tyr Thr Phe Val Asn Glu Asp Val 2850 2855 2860
- Gly Thr Ile Lys Pro Val Leu Gly Glu Arg Val Ile Pro Asp Pro Val 2865 2870 2875 2880
- Val Asp Ile Asn Leu Gln Pro Glu Val Gln Val Asp Thr Ser Glu Val 2885 2890 2895
- Gly Ile Thr Ile Ile Gly Arg Glu Thr Leu Met Thr Thr Gly Val Thr 2900 2905 2910
- Pro Val Leu Glu Lys Val Glu Pro Asp Ala Ser Asp Asn Gln Asn Ser 2915 2920 2925
- Val Lys Ile Gly Leu Asp Glu Gly Asn Tyr Pro Gly Pro Gly Ile Gln 2930 2935 2940
- Thr His Thr Leu Thr Glu Glu Ile His Asn Arg Asp Ala Arg Pro Phe 2945 2950 2955 2960
- Ile Met Ile Leu Gly Ser Arg Asn Ser Ile Ser Asn Arg Ala Lys Thr
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- Ala Arg Asn Ile Asn Leu Tyr Thr Gly Asn Asp Pro Arg Glu Ile Arg 2980 2985 2990
- Asp Leu Met Ala Ala Gly Arg Met Leu Val Val Ala Leu Arg Asp Val 2995 3000 3005
- Asp Pro Glu Leu Ser Glu Met Val Asp Phe Lys Gly Thr Phe Leu Asp 3010 3015 3020
- Arg Glu Ala Leu Glu Ala Leu Ser Leu Gly Gln Pro Lys Pro Lys Gln 3025 3030 3040
- Val Thr Lys Glu Ala Val Arg Asn Leu Ile Glu Gln Lys Lys Asp Val 3045 3050 3055
- Glu Ile Pro Asn Trp Phe Ala Ser Asp Asp Pro Val Phe Leu Glu Val 3060 3065 3070
- Ala Leu Lys Asn Asp Lys Tyr Tyr Leu Val Gly Asp Val Gly Glu Val
 3075 3080 3085



- Lys Asp Gln Ala Lys Ala Leu Gly Ala Thr Asp Gln Thr Arg Ile Ile 3090 3095 3100
- Lys Glu Val Gly Ser Arg Thr Tyr Ala Met Lys Leu Ser Ser Trp Phe 3105 3110 3115 3120
- Leu Gln Ala Ser Asn Lys Gln Met Ser Leu Thr Pro Leu Phe Glu Glu 3125 3130 3135
- Leu Leu Leu Arg Cys Pro Pro Ala Thr Lys Ser Asn Lys Gly His Met 3140 3145 3150
- Ala Ser Ala Tyr Gln Leu Ala Gln Gly Asn Trp Glu Pro Leu Gly Cys 3155 3160 3165
- Gly Val His Leu Gly Thr Ile Pro Ala Arg Arg Val Lys Ile His Pro 3170 3175 3180
- Tyr Glu Ala Tyr Leu Lys Leu Lys Asp Phe Ile Glu Glu Glu Glu Lys 3185 3190 3195 3200
- Lys Pro Arg Val Lys Asp Thr Val Ile Arg Glu His Asn Lys Trp Ile 3205 3210 3215
- Leu Lys Lys Ile Arg Phe Gln Gly Asn Leu Asn Thr Lys Lys Met Leu 3220 3225 3230
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- Arg Leu Glu Lys Leu Pro Ile Val Arg Ala Gln Thr Asp Thr Lys Thr 3265 3270 3275 3280
- Phe His Glu Ala Ile Arg Asp Lys Ile Asp Lys Ser Glu Asn Arg Gln 3285 3290 3295
- Asn Pro Glu Leu His Asn Lys Leu Leu Glu Ile Phe His Thr Ile Ala 3300 3305 3310
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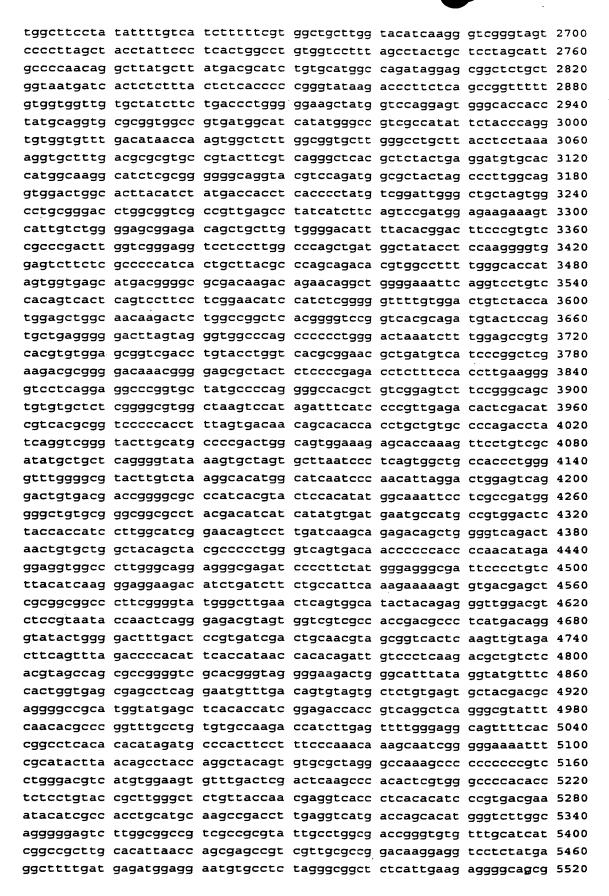
- Asn Ile Gly Glu Val Leu Asp Ser Glu Lys His Leu Val Glu Gln Leu 3345 3350 3355 3360
- Val Arg Asp Leu Lys Ala Gly Arg Lys Ile Lys Tyr Tyr Glu Thr Ala 3365 3370 3375
- Ile Pro Lys Asn Glu Lys Arg Asp Val Ser Asp Asp Trp Gln Ala Gly
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- Asp Leu Val Val Glu Lys Arg Pro Arg Val Ile Gln Tyr Pro Glu Ala 3395 3400 3405
- Lys Thr Arg Leu Ala Ile Thr Lys Val Met Tyr Asn Trp Val Lys Gln 3410 3415 3420
- Gln Pro Val Val Ile Pro Gly Tyr Glu Gly Lys Thr Pro Leu Phe Asn 3425 3430 3435 3440
- Ile Phe Asp Lys Val Arg Lys Glu Trp Asp Ser Phe Asn Glu Pro Val 3445 3450 3455
- Ala Val Ser Phe Asp Thr Lys Ala Trp Asp Thr Gln Val Thr Ser Lys 3460 3465 3470
- Asp Leu Gln Leu Ile Gly Glu Ile Gln Lys Tyr Tyr Tyr Lys Lys Glu 3475 3480 3485
- Trp His Lys Phe Ile Asp Thr Ile Thr Asp His Met Thr Glu Val Pro 3490 3495 3500
- Val Ile Thr Ala Asp Gly Glu Val Tyr Ile Arg Asn Gly Gln Arg Gly 3505 3510 3515 3520
- Ser Gly Gln Pro Asp Thr Ser Ala Gly Asn Ser Met Leu Asn Val Leu 3525 3530 3535
- Thr Met Met Tyr Ala Phe Cys Glu Ser Thr Gly Val Pro Tyr Lys Ser 3540 3545 3550
- Phe Asn Arg Val Ala Arg Ile His Val Cys Gly Asp Asp Gly Phe Leu 3555 3560 3565
- Ile Thr Glu Lys Gly Leu Gly Leu Lys Phe Ala Asn Lys Gly Met Gln 3570 3575 3580
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- Met Lys Val Ala Tyr Arg Phe Glu Asp Ile Glu Phe Cys Ser His Thr 3605 3610 3615
- Pro Val Pro Val Arg Trp Ser Asp Asn Thr Ser Ser His Met Ala Gly
 3620 3625 3630
- Arg Asp Thr Ala Val Ile Leu Ser Lys Met Ala Thr Arg Leu Asp Ser 3635 3640 3645
- Ser Gly Glu Arg Gly Thr Thr Ala Tyr Glu Lys Ala Val Ala Phe Ser 3650 3655 3660
- Phe Leu Leu Met Tyr Ser Trp Asn Pro Leu Val Arg Arg Ile Cys Leu 3665 3670 3680
- Leu Val Leu Ser Gln Gln Pro Glu Thr Asp Pro Ser Lys His Ala Thr 3685 3690 3695
- Tyr Tyr Tyr Lys Gly Asp Pro Ile Gly Ala Tyr Lys Asp Val Ile Gly 3700 3705 3710
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- Leu Asn Leu Ser Leu Ser Thr Leu Gly Ile Trp Thr Lys His Thr Ser 3730 3735 3740
- Lys Arg Ile Ile Gln Asp Cys Val Ala Ile Gly Lys Glu Glu Gly Asn 3745 3750 3755 3760
- Trp Leu Val Asn Ala Asp Arg Leu Ile Ser Ser Lys Thr Gly His Leu 3765 3770 3775
- Tyr Ile Pro Asp Lys Gly Phe Thr Leu Gln Gly Lys His Tyr Glu Gln 3780 3785 3790
- Leu Gln Leu Arg Thr Glu Thr Asn Pro Val Met Gly Val Gly Thr Glu 3795 3800 3805
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Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro 50 55 60

Ile Pro Lys Asp Arg Arg Ser Thr Gly Lys Ser Trp Gly Lys Pro Gly 65 70 75 80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp
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- Arg His Arg Ser Arg Asn Val Gly Lys Val Ile Asp Thr Leu Thr Cys
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- Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp 145 150 155 160
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- Pro Val Ser Pro Asn Val Ala Val Gln Arg Pro Gly Ala Leu Thr Gln 245 250 255
- Gly Leu Arg Thr His Ile Asp Met Val Val Met Ser Ala Thr Leu Cys 260 265 270
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- Arg Pro Pro Leu Gly Ser Trp Phe Gly Cys Thr Trp Met Asn Ser Ser 545 550 555 560
- Gly Tyr Thr Lys Thr Cys Gly Ala Pro Pro Cys Arg Thr Arg Ala Asp 565 570 575
- Phe Asn Ala Ser Thr Asp Leu Leu Cys Pro Thr Asp Cys Phe Arg Lys 580 585 590
- His Pro Asp Thr Thr Tyr Leu Lys Cys Gly Ser Gly Pro Trp Leu Thr
 595 600 605





Pro Arg Cys Leu Ile Asp Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys 610 620

Thr Val Asn Tyr Thr Ile Phe Lys Ile Arg Met Tyr Val Gly Gly Val 625 630 635 640

Glu His Arg Leu Thr Ala Ala Cys Asn Phe Thr Arg Gly Asp Arg Cys 645 650 655

Asn Leu Glu Asp Arg Asp Arg Ser Gln Leu Ser Pro Leu Leu His Ser 660 665 670

Thr Thr Glu Trp Ala Ile Leu Pro Cys Ser Tyr Ser Asp Leu Pro Ala 675 680 685

Leu Ser Thr Gly Leu Leu His Leu His Gln Asn Ile Val Asp Val Gln 690 695 700

Phe Met Tyr Gly Leu Ser Pro Ala Leu Thr Lys Tyr Ile Val Arg Trp 705 710 715 720

Glu Trp Val Ile Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Val Cys
725 730 735

Ala Cys Leu Trp Met Leu Ile Leu Leu Gly Gln Ala Glu Ala Ala Leu
740 745 750

Glu Lys Leu Val Ile Leu His Ala Ala Ser Ala Ala Ser Cys Asn Gly
755 760 765

Phe Leu Tyr Phe Val Ile Phe Phe Val Ala Ala Trp Tyr Ile Lys Gly 770 775 780

Arg Val Val Pro Leu Ala Thr Tyr Ser Leu Thr Gly Leu Trp Ser Phe 785 790 795 800

Ser Leu Leu Leu Leu Ala Leu Pro Gln Gln Ala Tyr Ala Tyr Asp Ala 805 810 815

Ser Val His Gly Gln Ile Gly Ala Ala Leu Leu Val Met Ile Thr Leu 820 825 830

Phe Thr Leu Thr Pro Gly Tyr Lys Thr Leu Leu Ser Arg Phe Leu Trp 835 840 845

Trp Leu Cys Tyr Leu Leu Thr Leu Gly Glu Ala Met Val Gln Glu Trp 850 855 860





Ala Pro Pro Met Gln Val Arg Gly Gly Arg Asp Gly Ile Ile Trp Ala 865 870 875 880

Val Ala Ile Phe Tyr Pro Gly Val Val Phe Asp Ile Thr Lys Trp Leu 885 890 895

Leu Ala Val Leu Gly Pro Ala Tyr Leu Leu Lys Gly Ala Leu Thr Arg
900 905 910

Val Pro Tyr Phe Val Arg Ala His Ala Leu Leu Arg Met Cys Thr Met 915 920 925

Ala Arg His Leu Ala Gly Gly Arg Tyr Val Gln Met Ala Leu Leu Ala 930 935 940

Leu Gly Arg Trp Thr Gly Thr Tyr Ile Tyr Asp His Leu Thr Pro Met 945 950 955 960

Ser Asp Trp Ala Ala Ser Gly Leu Arg Asp Leu Ala Val Ala Val Glu 965 970 975

Pro Ile Ile Phe Ser Pro Met Glu Lys Lys Val Ile Val Trp Gly Ala 980 985 990

Glu Thr Ala Ala Cys Gly Asp Ile Leu His Gly Leu Pro Val Ser Ala 995 1000 1005

Arg Leu Gly Arg Glu Val Leu Leu Gly Pro Ala Asp Gly Tyr Thr Ser 1010 1015 1020

Lys Gly Trp Ser Leu Leu Ala Pro Ile Thr Ala Tyr Ala Gln Gln Thr 1025 1030 1035 1040

Arg Gly Leu Leu Gly Thr Ile Val Val Ser Met Thr Gly Arg Asp Lys
1045 1050 1055

Thr Glu Gln Ala Gly Glu Ile Gln Val Leu Ser Thr Val Thr Gln Ser 1060 1065 1070

Phe Leu Gly Thr Ser Ile Ser Gly Val Leu Trp Thr Val Tyr His Gly 1075 1080 1085

Ala Gly Asn Lys Thr Leu Ala Gly Ser Arg Gly Pro Val Thr Gln Met 1090 1095 1100

Tyr Ser Ser Ala Glu Gly Asp Leu Val Gly Trp Pro Ser Pro Pro Gly 1105 1110 1115 1120



- Thr Lys Ser Leu Glu Pro Cys Thr Cys Gly Ala Val Asp Leu Tyr Leu 1125 1130 1135
- Val Thr Arg Asn Ala Asp Val Ile Pro Ala Arg Arg Arg Gly Asp Lys
 1140 1145 1150
- Arg Gly Ala Leu Leu Ser Pro Arg Pro Leu Ser Thr Leu Lys Gly Ser 1155 1160 1165
- Ser Gly Gly Pro Val Leu Cys Pro Arg Gly His Ala Val Gly Val Phe 1170 1175 1180
- Arg Ala Ala Val Cys Ser Arg Gly Val Ala Lys Ser Ile Asp Phe Ile 1185 1190 1195 1200
- Pro Val Glu Thr Leu Asp Ile Val Thr Arg Ser Pro Thr Phe Ser Asp 1205 1210 1215
- Asn Ser Thr Pro Pro Ala Val Pro Gln Thr Tyr Gln Val Gly Tyr Leu 1220 1225 1230
- His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Val Ala Tyr 1235 1240 1245
- Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala 1250 1255 1260
- Thr Leu Gly Phe Gly Ala Tyr Leu Ser Lys Ala His Gly Ile Asn Pro 1265 1270 1275 1280
- Asn Ile Arg Thr Gly Val Arg Thr Val Thr Thr Gly Ala Pro Ile Thr 1285 1290 1295
- Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ala Gly Gly
 1300 1310
- Ala Tyr Asp Ile Ile Ile Cys Asp Glu Cys His Ala Val Asp Ser Thr 1315 1320 1325
- Thr Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly
 1330 1335 1340
- Val Arg Leu Thr Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr 1345 1350 1355 1360
- Thr Pro His Pro Asn Ile Glu Glu Val Ala Leu Gly Gln Glu Gly Glu 1365 1370 1375





- Ile Pro Phe Tyr Gly Arg Ala Ile Pro Leu Ser Tyr Ile Lys Gly Gly
 1380 1385 1390
- Arg His Leu Ile Phe Cys His Ser Lys Lys Cys Asp Glu Leu Ala 1395 1400 1405
- Ala Ala Leu Arg Gly Met Gly Leu Asn Ser Val Ala Tyr Tyr Arg Gly 1410 1415 1420
- Leu Asp Val Ser Val Ile Pro Thr Gln Gly Asp Val Val Val Val Ala 1425 1430 1435 1440
- Thr Asp Ala Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile 1445 1450 1455
- Asp Cys Asn Val Ala Val Thr Gln Val Val Asp Phe Ser Leu Asp Pro 1460 1465 1470
- Thr Phe Thr Ile Thr Thr Gln Ile Val Pro Gln Asp Ala Val Ser Arg 1475 1480 1485
- Ser Gln Arg Arg Gly Arg Thr Gly Arg Gly Arg Leu Gly Ile Tyr Arg 1490 1495 1500
- Tyr Val Ser Thr Gly Glu Arg Ala Ser Gly Met Phe Asp Ser Val Val 1505 1510 1515 1520
- Leu Cys Glu Cys Tyr Asp Ala Gly Ala Ala Trp Tyr Glu Leu Thr Pro 1525 1530 1535
- Ser Glu Thr Thr Val Arg Leu Arg Ala Tyr Phe Asn Thr Pro Gly Leu 1540 1545 1550
- Pro Val Cys Gln Asp His Leu Glu Phe Trp Glu Ala Val Phe Thr Gly
 1555 1560 1565
- Leu Thr His Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ser Gly
 1570 1575 1580
- Glu Asn Phe Ala Tyr Leu Thr Ala Tyr Gln Ala Thr Val Cys Ala Arg 1585 1590 1595 1600
- Ala Lys Ala Pro Pro Pro Ser Trp Asp Val Met Trp Lys Cys Leu Thr 1605 1610 1615
- Arg Leu Lys Pro Thr Leu Val Gly Pro Thr Pro Leu Leu Tyr Arg Leu 1620 1625 1630



- Gly Ser Val Thr Asn Glu Val Thr Leu Thr His Pro Val Thr Lys Tyr 1635 1640 1645
- Ile Ala Thr Cys Met Gln Ala Asp Leu Glu Val Met Thr Ser Thr Trp 1650 1655 1660
- Val Leu Ala Gly Gly Val Leu Ala Ala Val Ala Ala Tyr Cys Leu Ala 1665 1670 1675 1680
- Thr Gly Cys Val Cys Ile Ile Gly Arg Leu His Ile Asn Gln Arg Ala 1685 1690 1695
- Val Val Ala Pro Asp Lys Glu Val Leu Tyr Glu Ala Phe Asp Glu Met 1700 1705 1710
- Glu Glu Cys Ala Ser Arg Ala Ala Leu Ile Glu Glu Gly Gln Arg Ile 1715 1720 1725
- Ala Glu Met Leu Lys Ser Lys Ile Gln Gly Leu Leu Gln Gln Ala Ser 1730 1735 1740
- Lys Gln Ala Gln Asp Ile Gln Pro Thr Val Gln Ala Ser Trp Pro Lys 1745 1750 1755 1760
- Val Glu Gln Phe Trp Ala Lys His Met Trp Asn Phe Ile Ser Gly Ile 1765 1770 1775
- Gln Tyr Leu Ala Gly Leu Ser Thr Leu Pro Gly Asn Pro Ala Val Ala 1780 1785 1790
- Ser Met Met Ala Phe Ser Ala Ala Leu Thr Ser Pro Leu Ser Thr Ser 1795 1800 1805
- Thr Thr Ile Leu Leu Asn Ile Leu Gly Gly Trp Leu Ala Ser Gln Ile 1810 1815 1820
- Ala Pro Pro Ala Gly Ala Thr Gly Phe Val Val Ser Gly Leu Val Gly 1825 1830 1835 1840
- Ala Ala Val Gly Ser Ile Gly Leu Gly Lys Val Leu Val Asp Ile Leu 1845 1850 1855
- Ala Gly Tyr Gly Ala Gly Ile Ser Gly Ala Leu Val Ala Phe Lys Ile 1860 1865 1870
- Met Ser Gly Glu Lys Pro Ser Met Glu Asp Val Val Asn Leu Leu Pro 1875 1880 1885





- Gly Ile Leu Ser Pro Gly Ala Leu Val Val Gly Val Ile Cys Ala Ala 1890 1895 1900
- Ile Leu Arg Arg His Val Gly Pro Gly Glu Gly Ala Val Gln Trp Met 1905 1910 1915 1920
- Asn Arg Leu Ile Ala Phe Ala Ser Arg Gly Asn His Val Ala Pro Thr 1925 1930 1935
- His Tyr Val Thr Glu Ser Asp Ala Ser Gln Arg Val Thr Gln Leu Leu 1940 1945 1950
- Gly Ser Leu Thr Ile Thr Ser Leu Leu Arg Arg Leu His Asn Trp Ile 1955 1960 1965
- Thr Glu Asp Cys Pro Ile Pro Cys Gly Gly Ser Trp Leu Arg Asp Val 1970 1975 1980
- Trp Asp Trp Val Cys Thr Ile Leu Thr Asp Phe Lys Asn Trp Leu Thr 1985 1990 1995 2000
- Ser Lys Leu Phe Pro Lys Met Pro Gly Leu Pro Phe Val Ser Cys Gln 2005 2010 2015
- Lys Gly Tyr Lys Gly Val Trp Ala Gly Thr Gly Ile Met Thr Thr Arg 2020 2025 2030
- Cys Pro Cys Gly Ala Asn Ile Ser Gly Asn Val Arg Leu Gly Ser Met 2035 2040 2045
- Arg Ile Thr Gly Pro Lys Thr Cys Met Asn Ile Trp Gln Gly Thr Phe 2050 2055 2060
- Pro Ile Asn Cys Tyr Thr Glu Gly Gln Cys Val Pro Lys Pro Ala Pro 2065 2070 2075 2080
- Asn Phe Lys Val Ala Ile Trp Arg Val Ala Ala Ser Glu Tyr Ala Glu 2085 2090 2095
- Val Thr Gln His Gly Ser Tyr His Tyr Ile Thr Gly Leu Thr Thr Asp 2100 2105 2110
- Asn Leu Lys Val Pro Cys Gln Leu Pro Ser Pro Glu Phe Phe Ser Trp 2115 2120 2125
- Val Asp Gly Val Gln Ile His Arg Phe Ala Pro Thr Pro Lys Pro Phe 2130 2135 2140





Phe Arg Asp Glu Val Ser Phe Cys Val Gly Leu Asn Ser Phe Val Val 2145 2150 2155 2160

Gly Ser Gln Leu Pro Cys Asp Pro Glu Pro Asp Thr Asp Val Leu Met 2165 2170 2175

Ser Met Leu Thr Asp Pro Ser His Ile Thr Ala Glu Thr Ala Ala Arg 2180 2185 2190

Arg Leu Ala Arg Gly Ser Pro Pro Ser Glu Ala Ser Ser Ser Ala Ser 2195 2200 2205

Gln Leu Ser Ala Pro Ser Leu Arg Ala Thr Cys Thr Thr His Gly Lys 2210 2215 2220

Ala Tyr Asp Val Asp Met Val Asp Ala Asn Leu Phe Met Gly Gly Asp 2225 2230 2235 2240

Val Thr Arg Ile Glu Ser Gly Ser Lys Val Val Leu Asp Ser Leu
2245 2250 2255

Asp Pro Met Val Glu Glu Arg Ser Asp Leu Glu Pro Ser Ile Pro Ser 2260 2265 2270

Glu Tyr Met Leu Pro Lys Lys Arg Phe Pro Pro Ala Leu Pro Ala Trp 2275 2280 2285

Ala Arg Pro Asp Tyr Asn Pro Pro Leu Val Glu Ser Trp Lys Arg Pro 2290 2295 2300

Asp Tyr Gln Pro Ala Thr Val Ala Gly Cys Ala Leu Pro Pro Pro Arg 2305 2310 2315 2320

Lys Thr Pro Thr Pro Pro Pro Arg Arg Arg Thr Val Gly Leu Ser 2325 2330 2335

Glu Asp Ser Ile Gly Asp Ala Leu Gln Gln Leu Ala Ile Lys Ser Phe 2340 2345 2350 $^{\circ}$

Gly Gln Pro Pro Pro Ser Gly Asp Ser Gly Leu Ser Thr Gly Ala Gly
2355 2360 2365

Ala Ala Asp Ser Gly Ser Gln Thr Pro Pro Asp Glu Leu Ala Leu Ser 2370 2375 2380

Glu Thr Gly Ser Ile Ser Ser Met Pro Pro Leu Glu Gly Glu Leu Gly 2385 2390 2395 2400





- Asp Pro Asp Leu Glu Pro Glu Gln Val Glu Pro Gln Pro Pro Pro Gln 2405 2410 2415
- Gly Gly Val Ala Ala Pro Gly Ser Asp Ser Gly Ser Trp Ser Thr Cys 2420 2425 2430
- Ser Glu Glu Asp Asp Ser Val Val Cys Cys Ser Met Ser Tyr Ser Trp 2435 2440 2445
- Thr Gly Ala Leu Ile Thr Pro Cys Ser Pro Glu Glu Glu Lys Leu Pro 2450 2455 2460
- Ile Asn Pro Leu Ser Asn Ser Leu Leu Arg Tyr His Asn Lys Val Tyr 2465 2470 2475 2480
- Cys Thr Thr Lys Ser Ala Ser Leu Arg Ala Lys Lys Val Thr Phe 2485 2490 2495
- Asp Arg Met Gln Val Leu Asp Ser Tyr Tyr Asp Ser Val Leu Lys Asp 2500 2505 2510
- Ile Lys Leu Ala Ala Ser Lys Val Thr Ala Arg Leu Leu Thr Met Glu 2515 2520 2525
- Glu Ala Cys Gln Leu Thr Pro Pro His Ser Ala Arg Ser Lys Tyr Gly 2530 2535 2540
- Phe Gly Ala Lys Glu Val Arg Ser Leu Ser Gly Arg Ala Val Asn His 2545 2550 2555 2560
- Ile Lys Ser Val Trp Lys Asp Leu Leu Glu Asp Ser Glu Thr Pro Ile 2565 2570 2575
- Pro Thr Thr Ile Met Ala Lys Asn Glu Val Phe Cys Val Asp Pro Thr
 2580 2585 2590
- Lys Gly Gly Lys Lys Ala Ala Arg Leu Ile Val Tyr Pro Asp Leu Gly 2595 2600 2605
- Val Arg Val Cys Glu Lys Met Ala Leu Tyr Asp Ile Thr Gln Lys Leu 2610 2615 2620
- Pro Gln Ala Val Met Gly Ala Ser Tyr Gly Phe Gln Tyr Ser Pro Ala 2625 2630 2635 2640
- Gln Arg Val Glu Phe Leu Leu Lys Ala Trp Ala Glu Lys Lys Asp Pro 2645 2650 2655



- Met Gly Phe Ser Tyr Asp Thr Arg Cys Phe Asp Ser Thr Val Thr Glu 2660 2665 2670
- Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr Arg Ala Cys Ser Leu Pro 2675 2680 2685
- Glu Glu Ala His Thr Ala Ile His Ser Leu Thr Glu Arg Leu Tyr Val 2690 2695 2700
- Gly Gly Pro Met Phe Asn Ser Lys Gly Gln Thr Cys Gly Tyr Arg Arg 2705 2710 2715 2720
- Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Met Gly Asn Thr Ile Thr 2725 2730 2735
- Cys Tyr Val Lys Ala Leu Ala Ala Cys Lys Ala Ala Gly Ile Ile Ala 2740 2745 2750
- Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val Val Ile Ser Glu Ser 2755 2760 2765
- Gln Gly Thr Glu Glu Asp Glu Arg Asn Leu Arg Ala Phe Thr Glu Ala 2770 2775 2780
- Met Thr Arg Tyr Ser Ala Pro Pro Gly Asp Pro Pro Arg Pro Glu Tyr 2785 2790 2795 2800
- Asp Leu Glu Leu Ile Thr Ser Cys Ser Ser Asn Val Ser Val Ala Leu 2805 2810 2815
- Gly Pro Gln Gly Arg Arg Tyr Tyr Leu Thr Arg Asp Pro Thr Thr 2820 2825 2830
- Pro Ile Ala Arg Ala Ala Trp Glu Thr Val Arg His Ser Pro Val Asn 2835 2840 2845
- Ser Trp Leu Gly Asn Ile Ile Gln Tyr Ala Pro Thr Ile Trp Ala Arg 2850 2855 2860
- Met Val Leu Met Thr His Phe Phe Ser Ile Leu Met Ala Gln Asp Thr 2865 2870 2875 2880
- Leu Asp Gln Asn Leu Asn Phe Glu Met Tyr Gly Ala Val Tyr Ser Val 2885 2890 2895
- Ser Pro Leu Asp Leu Pro Ala Ile Ile Glu Arg Leu His Gly Leu Asp 2900 2905 2910



Ala Phe Ser Leu His Thr Tyr Thr Pro His Glu Leu Thr Arg Val Ala 2915 2920 2925

Ser Ala Leu Arg Lys Leu Gly Ala Pro Pro Leu Arg Ala Trp Lys Ser 2930 2935 2940

Arg Ala Arg Ala Val Arg Ala Ser Leu Ile Ser Arg Gly Gly Arg Ala 2945 2950 2955 2960

Ala Val Cys Gly Arg Tyr Leu Phe Asn Trp Ala Val Lys Thr Lys Leu 2965 2970 2975

Lys Leu Thr Pro Leu Pro Glu Ala Arg Leu Leu Asp Leu Ser Ser Trp 2980 2985 2990

Phe Thr Val Gly Ala Gly Gly Gly Asp Ile Tyr His Ser Val Ser Arg 2995 3000 3005

Ala Arg Pro Arg Leu Leu Leu Phe Gly Leu Leu Leu Leu Phe Val Gly 3010 3015 3020

Val Gly Leu Phe Leu Leu Pro Ala Arg 3025 3030

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60/137,817 (CON) 4 June 1999 (04.06.1999)

(71) Applicant (for all designated States except US): THE GOVERNMENT OF THE UNITED STATES OF AMERICA as represented by THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES [US/US]; Office of Technology Transfer, National Institutes of Health, Suite 325, 6011 Executive Boulevard, Rockville, MD 20852 (US).

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- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
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Published:

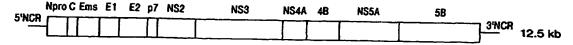
with international search report

(88) Date of publication of the international search report: 15 November 2001

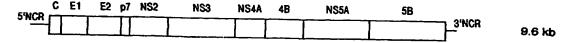
[Continued on next page]

(54) Title: HCV/BVDV CHIMERIC GENOMES AND USES THEREOF

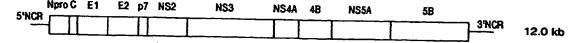
BVDV-NADL



HCV-H77C



HCV/BVDV (Chimeric RNA)



(57) Abstract: The present invention relates to molecular approaches to the production of nucleic acid sequences which comprise the genomes of chimeric hepatitis C virus-bovine viral diarrhea viruses (HCV-BVDV). The invention also relates to the use of these chimeric nucleic acid sequences to produce chimeric virions in cells and the use of these chimeric virions in HCV antibody neutralization assays, and for the development of vaccines and therapeutics for HCV.



O 00/75352 A3



For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

Int :tional Application No PCT/US 00/15527

			101/03 00/1				
A. CLASSI IPC 7	FICATION OF SUBJECT MATTER C12N15/86 C12N7/01 C07K14/	/18					
According to International Patent Classification (IPC) or to both national classification and IPC							
B. FIELDS SEARCHED							
Minimum do	ocumentation searched (classification system followed by classification C12N C07K	ation symbols)					
	tion searched other than minimum documentation to the extent that			hed			
	ata base consulted during the international search (name of data in tage). The properties of the search (name of data in tage). The properties of the properties of the search (name of data in the properties of	pase and, where practical, s	earch terms used)				
C. DOCUM	ENTS CONSIDERED TO BE RELEVANT						
Category °	Citation of document, with indication, where appropriate, of the r	elevant passages		Relevant to daim No.			
X	FROLOV I ET AL: "CIS-ACTING RNA ELEMENTS REQUIRED FOR REPLICATION OF BOVINE VIRAL DIARRHEA VIRUS-HEPATITIS C VIRUS 5' NONTRANSLATED REGION CHIMERAS" RNA, CAMBRIGDE UNIVERSITY PRESS, CAMBRIDGE, GB, vol. 4, no. 11, 25 November 1998 (1998-11-25), pages 1418-1435, XP000952790 ISSN: 1355-8382 the whole document /						
χ Furti	ner documents are listed in the continuation of box C.	X Patent family me	embers are listed in a	nnex.			
° Special ca	tegories of cited documents :	<u> </u>					
'A' docume consid 'E' earlier of filing d 'L' docume which citation 'O' docume other r 'P' docume later th	ant defining the general state of the art which is not elered to be of particular relevance document but published on or after the international late ent which may throw doubts on priority claim(s) or is cited to establish the publication date of another nor other special reason (as specified) ent referring to an oral disclosure, use, exhibition or means ent published prior to the international filing date but han the priority date claimed	or priority date and ricted to understand invention *X* document of particula cannot be considere involve an inventive *Y* document of particula cannot be considere document is combining ments, such combining the art. *&* document member of	ument of particular relevance; the claimed invention not be considered novel or cannot be considered to robve an inventive step when the document is taken alone ument of particular relevance; the claimed invention not be considered to involve an inventive step when the cument is combined with one or more other such docuents, such combination being obvious to a person skilled				
	actual completion of the international search	Date of mailing of the	Date of mailing of the international search report 1 4 02 2001				
	February 2001		I 4%, ₹	12, 4001			
Name and n	nailing address of the ISA European Palent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Authorized officer Chambonn	Authorized officer Chambonnet, F				

Int tional Application No
PCT/US 00/15527

Category °	ation) DOCUMENTS CONSIDERED TO BE RELEVANT	
Calegory	Citation of document, with indication, where appropriate, of the relevant passages	Delevent de la
	Chanon of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	H LU ET AL: "Poliovirus chimeras replicating under the translation control of genetic elements of HCV reveal unusual properties of the IRES of HCV" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, NATIONAL ACADEMY OF SCIENCE. WASHINGTON, US, vol. 93, February 1996 (1996-02), pages 1412-1417, XP002919370 ISSN: 0027-8424 the whole document	12,13
X	VENUGOPAL K. & GOULD E.A.: "Towards a new generation of Flavivirus vaccines" VACCINE, vol. 2, no. 11, 1994, pages 966-975, XP002919372 GUILDFORD GB the whole document	11,12,20
Ρ,Χ	WO 99 55366 A (FROLOV ILYA ; MCBRIDE M SCOTT (US); RICE CHARLES M (US); UNIV WASHI) 4 November 1999 (1999-11-04) page 4, line 21 - line 30 page 10, line 31 -page 11, line 17 page 11, line 33 -page 15, line 8; claims 1-10,16-21; figures 21,25,26; examples 1,2,4,5	1,2,7,8, 14-21
A	MEYERS G ET AL: "RECOVERY OF CYTOPATHOGENIC AND NONCYTOPATHOGENIC BOVINE VIRAL DIARRHEA VIRUSES FROM CDNA CONSTRUCTS" JOURNAL OF VIROLOGY, THE AMERICAN SOCIETY FOR MICROBIOLOGY, US, vol. 70, no. 12, December 1996 (1996-12), pages 8606-8613, XP000952807 ISSN: 0022-538X the whole document	
А	YU H ET AL: "SEQUENCE AND STRUCTURAL ELEMENTS AT THE 3' TERMINUS OF BOVINE VIRALDIARRHEA VIRUS GENOMIC RNA: FUNCTIONAL ROLE DURING RNA REPLICATION" JOURNAL OF VIROLOGY, THE AMERICAN SOCIETY FOR MICROBIOLOGY, US, vol. 73, no. 5, May 1999 (1999-05), pages 3638-3648, XP000946998 ISSN: 0022-538X the whole document ———	7
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Int. tional Application No
PCT/US 00/15527

		PC1/US 00/1552/				
	(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT					
Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.				
T	LAI VC, ZHONG W, SKELTON A, INGRAVALLO P, VASSILEV V, DONIS RO, HONG Z, LAU JY: "Generation and characterization of a hepatitis C virus NS3 protease-dependent bovine viral diarrhea virus." JOURNAL OF VIROLOGY., vol. 74, no. 14, July 2000 (2000-07), pages 6339-6347, XPO00952808 THE AMERICAN SOCIETY FOR MICROBIOLOGY., US ISSN: 0022-538X the whole document	7,8				

2

International application No. PCT/US 00/15527

B x I Observations wher certain claims w re found uns archabl (Continuation of it m 1 of first she t)
This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:
Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:
2. Claims Nos.: because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).
B x II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)
This International Searching Authority found multiple inventions in this international application, as follows:
see additional sheet
As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
Remark on Protest The additional search fees were accompanied by the applicant's protest. X No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-6 11-13 partially 9, 10, 14-21

A nucleic acid molecule comprising a chimeric virus genome, said genome being a BVDV genome in which the structural region of the BVDV genome has been replaced by the structural region of a hepatitis C virus genome; a DNA construct comprising said molecule; an RNA transcript of said DNA construct; a host cell transfected with said DNA construct or RNA transcript; a chimeric HCV-BVDV produced by said host cell; a composition comprising said virus.

2. Claims: 7, 8 and partially 9, 10, 14-21

A nucleic acid molecule comprising a chimeric virus genome, said genome being a BVDV genome in which the non-structural region of the BVDV genome has been replaced by the non-structural region of a hepatitis C virus genome; a DNA construct comprising said molecule; an RNA transcript of said DNA construct; a host cell transfected with said DNA construct or RNA transcript; a chimeric HCV-BVDV produced by said host cell; a composition comprising said virus.

Information on patent family members

Int tional Application No
PCT/US 00/15527

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
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